

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 21, 2004, 08:45:56 ; Search time 23.5 seconds
(without alignments)
8919.210 Million cell updates/sec

Title: US-09-602-362B-15

Perfect score: 3403

Sequence: 1 cccgtgcgttaagatggt.....gaaaaaaaaaaaaaaaaa 2030

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents AA -QFMT=fastan -SUFFIX=721.ra -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=35
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3261	95.8	1002	4	US-09-620-405B-475 Sequence 475, App
2	3261	95.8	1002	4	US-09-604-287A-475 Sequence 475, App
3	3261	95.8	1002	4	US-09-834-759-475 Sequence 475, App
4	3261	95.8	1095	4	US-09-620-405B-493 Sequence 493, App
5	3261	95.8	1095	4	US-09-834-759-493 Sequence 493, App
6	2184	64.2	445	4	US-09-620-405B-473 Sequence 473, App
7	2184	64.2	445	4	US-09-433-826B-473 Sequence 473, App
8	2184	64.2	445	4	US-09-604-287A-473 Sequence 473, App
9	2184	64.2	445	4	US-09-834-759-473 Sequence 473, App
10	2017	59.3	432	4	US-09-389-681-181 Sequence 181, App
11	2017	59.3	432	4	US-09-620-405B-181 Sequence 181, App
12	2017	59.3	432	4	US-09-339-338-181 Sequence 181, App

13	2017	59.3	432	4	US-09-433-826B-181	Sequence 181, App
14	2017	59.3	432	4	US-09-604-287A-181	Sequence 181, App
15	2017	59.3	432	4	US-09-285-480-181	Sequence 181, App
16	2017	59.3	432	4	US-09-834-759-181	Sequence 181, App
17	1597.5	46.9	650	4	US-09-620-405B-469	Sequence 469, App
18	1597.5	46.9	650	4	US-09-433-826B-469	Sequence 469, App
19	1597.5	46.9	650	4	US-09-604-287A-469	Sequence 469, App
20	1597.5	46.9	650	4	US-09-834-759-469	Sequence 469, App
21	1597.5	46.9	743	4	US-09-620-405B-494	Sequence 494, App
22	1597.5	46.9	743	4	US-09-834-759-494	Sequence 494, App
23	1404.5	41.3	410	4	US-09-620-405B-495	Sequence 495, App
24	1404.5	41.3	410	4	US-09-834-759-495	Sequence 495, App
25	1397	41.1	317	4	US-09-389-681-176	Sequence 176, App
26	1397	41.1	317	4	US-09-620-405B-176	Sequence 176, App
27	1397	41.1	317	4	US-09-339-338-176	Sequence 176, App
28	1397	41.1	317	4	US-09-433-826B-176	Sequence 176, App
29	1397	41.1	317	4	US-09-604-287A-176	Sequence 176, App
30	1397	41.1	317	4	US-09-285-480-176	Sequence 176, App
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32	1397	41.1	323	4	US-09-620-405B-483	Sequence 483, App
33	1397	41.1	323	4	US-09-604-287A-483	Sequence 483, App
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35	1070.5	31.5	466	4	US-09-620-405B-472	Sequence 472, App
36	1070.5	31.5	466	4	US-09-433-826B-472	Sequence 472, App
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44	847.5	24.9	179	4	US-09-285-480-179	Sequence 179, App
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ALIGNMENTS

RESULT 1

US-09-620-405B-475
; Sequence 475, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiaang, Yuglu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 475
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1002)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-405B-475

Alignment Scores:
Pred. No.: 2,51e-300 Length: 1002
Score: 3261.00 Matches: 654
Percent Similarity: 97.19% Conservative: 3
Best Local Similarity: 96.75% Mismatches: 15
Query Match: 95.83% Indels: 5
DB: 4 Gaps: 0

US-09-602-362E-15' (1-2030) x US-09-620-405B-475 (1-1002)

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Db |||||
347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGlnLysProSerAlaPhe 366
QY 129 GAGCTGCCATTGAAATGCAAAAGTCTGTCCAAATAAAGCCCTTGAATGAAGATGA 188
Db |||||
367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386
QY 189 CAAACATTGAGAGCAGATGAGTACTCCCATCAGAATCCAAACAAAGGAGCTATGAAGAA 248
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QY 249 AGTTCTTGGGATCTGAGACTCTCTGTGAGACTGTTTCACAGAGGATGTGTGTACCC 308
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Db |||||
427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446
QY 369 AATGATGGTTTTCTGAAGCTCCCTGAGAAATGAAAGTTTCTATTCCAACTAAGCCTTA 428
Db |||||
447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466
QY 429 GAATTGATGACATGCAAACTTTCAAAGCAGAGCCCTCCGAGAGGCATCTGCTTCGAG 488
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QY 1809 AGAATATTTCACCTCAAGCAAAATATGTGGCTTCAACAGCAATTAGTTCATCCAC 1868
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QY 1869 ATAANGAAGCTGCAACAAAGCAAGATACATATTCATTTCTTTGAGAGGAAA 1928
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QY 1929 ATGCN-CATCATCTTCTAAAGAGAAATGAGAGATATTTTNNATTCNATTAACCATTTA 1987
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966 MetGlnHisHisLeuLeuLysGluLysAsnGluIlePheAsnTyrAsnAsnHisLeu 985
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RESULT 2

US-09-604-287A-475
; Sequence 475, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.

APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C7

CURRENT APPLICATION NUMBER: US/09/604,287A

CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 489

SOFTWARE: Fast-Seq for Windows Version 3.0

SEQ ID NO 475

LENGTH: 1002

TYPE: PRT

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(1002)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-604-287A-475

Alignment Scores:

Pred. No.: 2,51e-300 Length: 1002
Score: 3261.00 Matches: 654
Percent Similarity: 97.19% Conservative: 3
Best Local Similarity: 96.75% Mismatches: 15
Query Match: 95.83% Indels: 5
DB: 4 Gaps: 0

US-09-602-362B-15 (1-2030) x US-09-604-287A-475 (1-1002)

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347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 366
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367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386
189 CAAACATTCAGACGATGAGATCTCCATCAGAAATCCAAACAAAGACCTATGAAGAA 248
387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 406
249 AGTCTTGGGATCTCAGAGTCTCTGTGAGACTGTTCACAGAGGATGTGTGTACCC 308
407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426
309 AAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATTAAGAAGTCTCCTGAT 368
427 LysAla**HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446
369 AATGATGTTTCTGAAAGCTCCCTGAGATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466
429 GAATTGATGCATGCAATCTTCAAGCAGAGCTCCCGAAGCCATCTGCTTCGAG 488
467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486
489 CTGCGAATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGAATGGAATGAAGAA 548
487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506
549 ACATTGAGAGCAGATCAGATGTTCTCTCAGAAATCAAAACAAAGAGTTCAAGAAAT 608
507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys**ValGluGluAsn 526
609 TCTGGGATCTCAGAGTCTCCGTGAGACTGTTCACAGAGGATGTGTGTACCCCAAG 668
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QY 729 TCAAAATCTTTGGATACAGTTTCATTCTTTGTAAGACAGCAAGGGAACCTCAAAAGATCAC 788
Db 567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586
QY 789 TGTGAACAACGTACAGGAAATCGAACAAATGAAAGAAAGAGTTTGTGACTGAAAG 848
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QY 849 AAACCTGTCAAGCAAAAGAAATATAATCAAGTTAGAGAACCAAAAGATTAAATGGGAA 908
Db 607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626
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Db 627 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAla 646
QY 969 CATATATTAAATGAAAAATTTAGGAAAGAAATAGCAAGAAATCGAAGACGACATAGGAAA 1028
Db 647 AspileLeuAsnGluLysIleArgGluLeuGluGlyArgIleGluGluGlnHisArgLys 666
QY 1029 GAGTTAGAGTGAACCAACTTGAACAGCTCTCAGATACAGATATAGAAATTTGAAG 1088
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QY 1329 TCTCAATATAGTGGCAGCTTAAAGTTCTCATAGCTGAGACACAAATGCTCACTTCTAAA 1388
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QY 1449 CTGCTTCTGCTGTACAGACCATGATCAAAATTTGTGACATCAAGAAATCTCAAGAACCT 1508
Db 807 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 826
QY 1509 GCTTTCCACATTCAGGAGATGCTTTGTTCCAAAGAAAAATGAATGTTGATGTGAGTAGT 1568
Db 827 AlaPheHisIleAlaGlyAspAlaCysLeuGluArgLysMetAsnValAspValSerSer 846
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Db 847 Thr-IleTyrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLys 866
QY 1629 AAGCTAAAAATTAATCTCAATTATCCAGGAGATGCTTAAGAGAAATACATTTGTTTC 1688
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QY 1689 AGGAACATGCACAAAGAGACCAACGTGAAACACAGATGTCAAATGAAGAGCTGAACACA 1748
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QY 1389 TTGAAGGAAAAACAAGCAAGAAATATAGAGCGAGAAATGAATCAACACCATCTCAGA 1448
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Db 807 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 826
QY 1509 GCTTTCCACATTCAGAGATGCTGTTTCCAAAGAAAAATGAATTTGATGTAGTACT 1568
Db 827 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSer 846
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QY 1629 AAGCCTAAAAATTAATCTCAATATATGAGAGATGCTCTAAGAGAAAAATACATTTGTTTC 1688
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Db 906 etTyrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 926
QY 1809 AGAAATATTTCAACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAGTTCATGCAC 1868
Db 926 InLysLeuPheGlnLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaH 946
QY 1869 ATAAGAAGAGCTGACACAAAGACGATGAAACATGATGATGATGATGATGATGATGATG 1928
Db 946 le-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 965
QY 1929 ATGCN-CATCATCTCTTAAAGAGAAAAATGAGGAGATATTTNATACNATACCATTTA 1987
Db 966 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeu 985
QY 1988 AAAAACCCTATATTCATATGGAAGAAAAAANAANAANAANAANAANAANAANAANAANA 2027
Db 986 LysAsn-ArgIleTyrGlnTyrGluLysGluLysAlaGlu 998
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RESULT 4

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US-09-620-405B-493
; Sequence 493, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 1095
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
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LOCATION: (1)....(1095)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-620-405B-493
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Alignment Scores:

		2,59e-300	Length:	1095
Score:		3261.00	Matches:	654
Percent Similarity:		97.19%	Conservative:	3
Best Local Similarity:		96.75%	Mismatches:	15
Query Match:		95.83%	Indels:	5
DB:		4	Gaps:	0

US-09-602-362E-15 (1-2030) x US-09-620-405B-493 (1-1095)

QY	9	GTAAAGATGCTCTCTGAAGGCTAACTCGGGAATGAAGTTCTTATTTCCAACTAAGACC	68
Db	420	VallysaspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla	439
QY	69	TTAGAAATGTAGCATGCACAACTTTCAAAGCAGAGCTCCCGAGAGACCATCTGCCTTC	128
Db	440	LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe	459
QY	129	GAGCTGCCATTGAATGCCAAAGTCTGTTCCTCAATTAAGCTTGGAAATGAAGAAATGAA	188
Db	460	GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu	479
QY	189	CAAACTTGTAGCAGCAGATGAGATATCTCCCATCAGAAATCCAAACAAAAAGGACTATGA	248
Db	480	GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu	499
QY	249	AGTTCTTGGGATTCGTAGAGTCTCTGTGAGACTCTTTCACAGAAAGGATGTGTGTACCC	308
Db	500	SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro	519
QY	309	AAGCTACACATCAAAAGAAATAGATAAATAATGAAATAGAGAGTCTCTCTGAT	368
Db	520	LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluLysSerProAsp	539
QY	369	AATCATGTTTCTGAAGGCTCCTCGAGAAATGAAGTATTTCTATTTCCAACTAAGACCTTA	428
Db	540	AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu	559
QY	429	GAATGTAGCAGCAGCAAACTTTCAAAGCAGAGCTCCCGAGAGACCATCTGCCTTCGAG	488
Db	560	GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu	579
QY	489	CCTGCCATTGAATGCAAAAGTCTGTTCCTCAATTAAGCCTTGGAAATGAAGAAATGAACA	548
Db	580	ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLysAsnGluGln	599
QY	549	ACATTGAGCAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAAAGAGGTGAAGAAAT	608
Db	600	ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn	619
QY	609	TCCTTGGGATTTCTGAGAGTCTCCGTGACACTGTTTTCACAGAAAGGATGTGTGTACCCAAG	668
Db	620	SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys	639
QY	669	GCTACACATCAAAAGAAATGGATAAATAAGTGGAAAAATAGAAATTCACACTAGCCTTA	728
Db	640	AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu	659
QY	729	TCAAAAATCTGGATACAGTTTCTTGTGAAAGAGCAAGGAACTTCAAAAAGATCAC	788
Db	660	SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis	679
QY	789	TGTGAAACAGCTACAGAAAAATGGAAACAAATGAAAGAAAGTGTGTGTACTGAAAGAG	848
Db	680	CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys	699
QY	849	AAACTGTGAGACCAAGAAATTAATACAGTGTAGAGAACCAAAAGTAATTCGAA	908
Db	700	LysLeuSerGluAlaLysGluIleLysSerGlnLeuGlnLysValLysTrpGlu	719

QY 909 CAAGAGCTCTGCACTGTGAGATTGACCTTTAAACCAAGAAAGAGAGAAATGATGCC 968
Db 720 GlnGluLeuCySerValArgLeuThrLeuAsnGlnGluGluGluLysArgAsnAla 739
QY 969 GATATATTAATCAAAATTTAGGAGAAATAGGAGAAATCGAGAGAGATAGGAAA 1028
Db 740 AspLeuAsnGluLysIleArgGluGluLeuGlyArgIleGluGlnHisArgLys 759
QY 1029 GAGTTAGAGTGAACCAACTTGACAGCTCTCAGAAATCAAGATATAGAAATGAAG 1088
Db 760 GluLeuGluValLysGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLys 779
QY 1089 AGTGTAGAAAGTAAATTGAATCAGGTTCTCACATCACTGAAATCAAAATATCTCTTA 1148
Db 780 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnThrLeuLeu 799
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Db 800 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 819
QY 1209 AAACACCAATACCAAGGAAAAAGAAATAATATCTTTGAGGACATTAAGATTTTAAAGAA 1268
Db 820 LysHisGlnThrGlnGluLysGluAsnLysThrPheGluAspIleLysLeuLysGlu 839
QY 1269 AAGAATCTGAATCTCAGATGACCTTAACTGAAAGAGGAATCATTAATAAGGGCA 1328
Db 840 LysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAla 859
QY 1329 TCTCAATATATAGTGGCAGCTTAAAGTTCTCATAGCTGAGAACCAATGCTCACTTAA 1388
Db 860 SerGlnThrSerGlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLys 879
QY 1389 TTGAGAGAAAAACAGCAAGAAATATCTAGAGGCAAGAAATCAATCAACACCTCTAG 1448
Db 880 LeuLysGluLysGlnAspLysGluIleLeuGluAlaGluIleGluSerHisThrProArg 899
QY 1449 CTGCTTCTGCTGTACAGACCATGATCAAAATGTGCATCAAGAAAAAGTCAAGAACCT 1508
Db 900 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 919
QY 1509 GCTTTCCACATTCAGAGAGATGCTTTTTCGAAAGAAATGAATGATGTGAGTACT 1568
Db 920 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSer 939
QY 1569 ACCGATATATAACAAATCAGAGTGTCCATCAACACATTTCTGAAGCTCAAGGAAATCCAN 1628
Db 940 Thr-IleThrAsnAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLys 959
QY 1629 AAGCTTAAAAATTAATCTCAATATGAGAGAGATGCTCTAAGAGAAATACATGCTTTC 1688
Db 959 sSerLeuLysIleAsnLeuAsnThrAlaGlyAspAlaLeuArgGluAsnThrLeuValSe 979
QY 1689 AGGAACATGCACAAGAGACCAAGCTCAACACACAGAGTGTCAAAATCAAGAAAGCTGAAACA 1748
Db 979 r-GluHisAlaGlnArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHis 999
QY 1749 TGTNTCAAANGCAACAAGATNATGTGAACAAACACACTGANCAGAGGAGTCTCTAGATC 1808
Db 999 etThrGlnAsnGluGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspG 1019
QY 1809 AGAATATTTCACTCAAGCAAGCAAAATATGTGGCTTCAACAGCAATTAAGTTTCATGCAAC 1868
Db 1019 InLysLeuPheGlnLeuGlnSerLysAsnMetThrLeuGlnGlnGlnLeuValHisAlaH 1039
QY 1869 ATAANGAAAGCTGCAACAAAGCAAGATATCAATTCATNTTCATNTTCCTTGAGAGGAAA 1928
Db 1039 is-LysLysAlaAspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLys 1058
QY 1929 ATGNC-CATCATCTCTTAAAGAGAAAAATCAGAGATATTTNATCATNATACCATTTA 1987
Db 1059 MetGlnHisHisLeuLeuLysGluLysAsnGluGluIlePheAsnThrAsnHisLeu 1078

QY 1988 AAAAACCCGTATATTTCATATATGAAAAAANAANAANA 2027
Db 1079 LysAsn-ArgIleThrGlnThrGluLysGluLysAlaGlu 1091
RESULT 5
US-09-834-759-493
; Sequence 493, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(1095)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-834-759-493
Alignment Scores:
Pred. No.: 2,59e-300 Length: 1095
Score: 3261.00 Matches: 654
Percent Similarity: 97.19% Conservative: 3
Best local Similarity: 96.75% Mismatches: 15
Query Match: 95.83% Indels: 5
DB: 4 Gaps: 0
US-09-602-362E-15 (1-2030) x US-09-834-759-493 (1-1095)
QY 9 GTTAAAGATGCTCTCTCAAGGCTAACTCGGATGAAGTTCTTATTCCAACTAAAGCC 68
Db 420 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 439
QY 69 TTAGAATTGATGGACATCGAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGCCTTC 128
Db 440 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 459
QY 129 GAGCTGCGCATTGAAATGCAAAAGTCTGTTCCAATAAGCTTGGATTAAGAGTAA 188
Db 460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479
QY 189 CAACATTGAGAGCAGATGAGATCTCCATCAGATTCCTCAACAAAGAGACTATGAAGA 248
Db 480 GlnThrLeuArgAlaAspGluIleuProSerGluSerLysGlnLysAspThrGluGlu 499
QY 249 AGTCTTGGGATCTGAGAGTCTCTGTGAGACTGTTTCACAGAGGATGTGTGTTTACCC 308
Db 500 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 519
QY 309 RAGGCTACACATCAAAAAGAAATAGATAAATAATGAAATAGAAAGAGTCTCTCGAT 368
Db 520 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 539
QY 369 AATGATGCTTTTGAAGGCTCCCTGCAAGATGAAGTTCCTTATTCACACTAAAGCCTTA 428
Db 540 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 559
QY 429 GAATGATGGACATGCAACTTCAAGCAGAGCTCCCGAGAGCCATCTGCCTTCGAG 488

Db 560 GluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPheGlu 579
QY 489 CTTGCCATTGAATGCAAAAGCTTGTCCAAATAAAGCCCTTGAATGGAAGTGAACAA 548
Db 580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLysAsnGluGln 599
QY 549 ACATTGAGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTCAAGAAAT 608
Db 600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619
QY 609 TCTTGGATTCTGAGAGTCTCCGTGAGACTGTTTCACAGAAGGATGTGTGTACCCCAAG 668
Db 620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639
QY 669 GCTTACACATCAAAAGAAATGATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 728
Db 640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659
QY 729 TCAAAATCTTGATACAGTTCATCTTCTGTAAGAGCAAGGAACTTCAAAAGATCAC 788
Db 660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679
QY 789 TGTGACACCTGACAGGAAATGACAAATGAAAGAAAGTGTGTGTGTGTGTGTGTGTGT 848
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QY 849 AAATCTGACAGCAAGAAATTAATACAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGT 908
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Db 720 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAla 739
QY 969 GATATATTAATGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAGGAAATTAAGG 1028
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QY 1089 AGTTAGAGAAATTAATGAGTTCAGTTCACCTCATGAAATGAAATTAATTAATCTCTTA 1148
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QY 1149 CATGAAATTCGATGTTGAAAGGAAATTCGATGCTAAAGTCAAGTCAAGTCAAGTCA 1208
Db 800 HisGluAsnCysMetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeu 819
QY 1209 AAACCAATACAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1268
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Db 840 LysAsnAlaGluLeuGlnMetThrLeuLysLeuLysGluLysLeuThrLysArgAla 859
QY 1329 TCTCAATATAGTGGGAGCTTAAATTCGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAA 1388
Db 860 SerGlnTyrSerGlyGlnLysValLeuIleAlaGluAsnThrMetLeuThrSerLys 879
QY 1389 TTGAAGGAAACAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1448
Db 880 LeuLysGluLysGlnAspLysGluLeuGluAlaGluIleGluSerHisProArg 899
QY 1449 CTGGCTTCTGTGTACAAGCATCATCAATTAATTAATTAATTAATTAATTAATTAATTA 1508
Db 900 LeuAlaSerAlaValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluPro 919
QY 1509 GCTTTCCATTCAGAGGAGCTGTTGTTGCAAGAAATTAATTAATTAATTAATTAATTA 1568
Db 920 AlaPheHisIleAlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSer 939

RESULT 6

US-09-620-405B-473
; Sequence 473, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 473
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-405B-473

Alignment Scores:
Pred. No.: 1,82e-198 Length: 445
Score: 2184.00 Matches: 427
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 64.18% Indels: 0
DB: 4 Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-620-405B-473 (1-445)

QY 9 GTTAAAGATGCTCTCTGAGGCTAACTGCGGAATGAAAGTTCTTATTCTCAACTAAGCC 68
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QY 69 TTGAATTTGATGACATGCAAACTTTCAAGAGAGCCCTCCGAGAGCATCTGCTTTC 128

Db 35 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 54
QY 129 GAGCCTGCCATTGAAATGCAAAAGTCTGTTCACAAATAAAGCCTTGAATGAAGATGAA 188
Db 55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74
QY 189 CAAACATTGAGACAGATGAGTACTCCCATCAGATCCAAACAAAGAGCATTGAAGAA 248
Db 75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspThrGluGlu 94
QY 249 AGTCTCTGGGATCTCAGAGTCTCTGTGAGTCTGTTTTCACAGAGGATCTGTTCACCC 308
Db 95 SerSerTrpAspSerGluSerLeuLysGluThrValSerGlnLysAspValCysLeuPro 114
QY 309 AAGCCTACACATCAAAAGAAATAGATTAATAATGGAATAGAAAGTCTCTGAT 368
Db 115 LysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluSerProAsp 134
QY 369 AATGATGGTCTTCTGAGGCTCCCTGCAGATGAAAGTCTTATTCCTCAACTAAAGCCTTA 428
Db 135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154
QY 429 GAATGATGACATGCAAACTTTCAAAGCAGACCTCCGAGAGCCTCTGCTTCGAG 488
Db 155 GluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPheGlu 174
QY 489 CCTGCCATTGCAAAATGCAAAAGTCTGTTCACAAATAAAGCCTTGGAAATGAAGATGAACA 548
Db 175 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194
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Db 195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysValGluGluAsn 214
QY 609 TCTTGGATTCAGAGTCTCCCTGAGCTGTTTCAAGAGGATGTTGTGACCCAG 668
Db 215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234
QY 669 GCTACACATCAAAAGAAATGGAATAAATGAAGTGAATAATGAAGATCAACTAGCCTTA 728
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QY 729 TCAAAATCTTGATACAGTCTCTTGTGAAGAGCAGGAGCTTCAAAAGATCAC 788
Db 255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274
QY 789 TGTGAACACGCTACAGGAAATGGAACAAATGAAAGAAAGTCTGTGCTACTGAAAGAA 848
Db 275 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysIlePheCysValLeuLysLys 294
QY 849 AACTGTGACAGCAAGAAATTAATACAGTGTAGAGCAACCAAAAGTTAAATGGGAA 908
Db 295 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 314
QY 909 CAAGAGCTCTGAGTGTGAGATGACTTTAAACCAAGAGCAAGAGAGAAATGCC 968
Db 315 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluLysArgAsnAla 334
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Db 335 AspileLeuAsnGluLysIleArgGluLeuGlyArgIleGluGlnHisArgLys 354
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QY 1149 CATCAAAATTCGATGTTGAAAGAAATTTGCCATGCTAAATCGAAATAGCACACTG 1208
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QY 1209 AATACCAATATCAGGAAAGGAAATAAATACTTTGAGGACATTAAAGATTTTAAAGAA 1268
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Db 435 LysAsnAlaGluLeuGlnMetThr 442

RESULT 7

US-09-433-826B-473
; Sequence 473, Application US/09433826B
; Patent No. 6579973

GENERAL INFORMATION:

; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433.826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 473
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-433-826B-473

Alignment Scores:
Pred. No.: 1,82e-198 Length: 445
Score: 2184.00 Matches: 427
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 64.18% Indels: 0
Gaps: 4

US-09-602-362E-15 (1-2030) x US-09-433-826B-473 (1-445)

QY 9 GTTAAAGATGCTCTCTCAAGGCTAAGTTCCTTCAAGTAAAGTTCCTTCAAGTAAAGCC 68
Db 15 VallyaspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 34
QY 69 TTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 128
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Db 55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74
QY 189 CAAACATTGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
Db 75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspThrGluGlu 94
QY 249 AGTCTCTGGGATCTCAGAGTCTCTGTGAGTCTGTTTTCACAGAGGATGTTGTTCACCC 308
Db 95 SerSerTrpAspSerGluSerLeuLysGluThrValSerGlnLysAspValCysLeuPro 114
QY 309 AAGCCTACACATCAAAAGAAATAGATTAATAATGGAATAGAAAGTCTCTGAT 368
Db 115 LysAlaAlaHisGlnLysGluIleAspLysIleAsnGlyLysLeuGluSerProAsp 134
QY 369 AATGATGGTCTTCTGAGGCTCCCTGCAGATGAAAGTCTTATTCCTCAACTAAAGCCTTA 428
Db 135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154
QY 429 GAATGATGACATGCAAACTTTCAAAGCAGACCTCCGAGAGCCTCTGCTTCGAG 488
Db 155 GluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPheGlu 174

489 CCTGCCATTCAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAATTAAGAAATGAACAA 548
175 ProAlaileGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194
549 ACATTGAGACGACATCAGATGTTCCCTTTCAGAAATCAAAACAAAGAGCTTGAAGAAAT 608
195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsn 214
609 TCTTGGATCTCAGAGTCTCCGTGAGAGCTGTTTCAAGAGAGTGTGTGTACCCAAAG 668
215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234
669 GCTACACATCAAAAGCAATGGAATAAATAAGTGAAGAAATTAAGATTCACACTAGCCTA 728
235 AlaThrHisGlnLysGluMetAspLysLysLysLysLysLysLysLysLysLysLys 254
729 TCAAAATCTTGATCAGTTCATCTTGTGAAGAGCAAGGAACTTCAAAAGATCAAC 788
255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274
789 TGTGAACAACGTACAGCAAAATGGAACAATCAAAAGAAAGTGTGTGTACTGAAAGAAG 848
275 CysGluGlnArgThrGlyLysMetGluMetLysLysLysLysLysLysLysLysLys 294
849 AAATCTCAGAACCAAAAGAAATAAATCACAGTTAGAGAACCAAAAGCTTAAATGGGAA 908
295 LysLeuSerGluAlaLysGluLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 314
909 CAAGACTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 968
315 GlnGluLeuCysSerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAla 334
969 GATATATTAAATGAAATTAAGGAAAGTAAAGGAAATGAGGAAATGAGGAAATGAGGAA 1028
335 AspIleLeuAsnGluLysLysLysLysLysLysLysLysLysLysLysLysLysLys 354
1029 GAGTTAGAAGTGAACCAACTGAAAGGCTTCAAGAGTGTGAGTGTGAGTGTGAGTGTGAG 1088
355 GluLeuGluValLysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLys 374
1089 AGTGTAGAAGTAATTTGAATCAGGTTCTCAGCTCATGAAATGAAATATCTCTTA 1148
375 SerValGluSerAsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeu 394
1149 CATGAAATGATGTTGAAAGGAAATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1208
395 HisGluAsnCysMetLeuLysLysLysLysLysLysLysLysLysLysLysLysLys 414
1209 AAACCCCAATACAGCAAGGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1268
415 LysHisGlnTyrGlnGlnLysGluAsnLysTyrPheGluAspIleLysLysLysLys 434
1269 AAGAATGCTGAATTCAGATGACC 1292
435 LysAsnAlaGluLeuGlnMetThr 442

RESULT 8
US-09-604-287A-473
Sequence 473, Application US/09604287A
Patent No. 6586572
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Repler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.470C7
CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 473
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
US-09-604-287A-473
Alignment Scores:
Pred. No.: 1,82e-198 Length: 445
Score: 2184.00 Matches: 427
Percent Similarity: 99.77% Conservative: 0
Best Local Similarity: 99.77% Mismatches: 1
Query Match: 64.18% Indels: 0
DB: 4 Gaps: 0
US-09-602-362E-15 (1-2030) x US-09-604-287A-473 (1-445)
QY 9 GTTAAAGATGCTCTTCTGAAGCTAACTCGGAATGAAGTTTCTATTCCAACCTAAAGCC 68
Db 15 VallyslaspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 34
QY 69 TTAGAATTGATGGACATGCCAACTTTCAAAGCAGAGCTCCCGAGAGCCATCTGCCTTC 128
Db 35 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPhe 54
QY 129 GAGCTGCTCAATTGAATGCCAAAGCTCTGTTCCAAATTAAGCCCTTGAATTAAGAAATGAA 188
Db 55 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 74
QY 189 CAAACATTGAGAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGAGCTATGAAGAA 248
Db 75 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyrGluGlu 94
QY 249 AGTTCTTGGGATTCGAGAGTCTCTGAGAGTCTGTTTCAAGAGGATGTGTGTACCC 308
Db 95 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 114
QY 309 AAGCTCACATCAAAAGAAATAGATAAATAAATAAATAAATAAATAAATAAATAAATAA 368
Db 115 LysAlaAlaHisGlnLysGluIleAspLysLysLysLysLysLysLysLysLysLys 134
QY 369 AATGATGGTTTCTGAAGGCTCCCTGCAGAAATGAAGTTTCTATTCCAACCTAAAGCCCTTA 428
Db 135 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 154
QY 429 GAATTGATGACATGCAAACTTTTCAAAGCAGAGCTCCCGAGAGCCATCTGCCTTCGAG 488
Db 155 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 174
QY 489 CTTCCCATTCAAATGCAAAAGTCTGTTCCAAATTAAGCCCTTGAATTAAGAAATGAACAA 548
Db 175 ProAlaileGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 194
QY 549 ACATTGAGACGACATCAGATGTTCCCTTCAAGATCAAAACAAAGAGCTTGAAGAAAT 608
Db 195 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLysLysValGluGluAsn 214
QY 609 TCTTGGGATTCGAGAGTCTCCGTGAGAGCTGTTTCAAGAGGATGTGTGTACCCAAAG 668
Db 215 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 234
QY 669 GCTACACATCAAAAGAAATGGAATAAATAAAGTGAAGAAATTAAGATTCACACTAGCCTA 728
Db 235 AlaThrHisGlnLysGluMetAspLysLysLysLysLysLysLysLysLysLysLys 254
QY 729 TCAAAATCTTGATCAGTTCATCTTGTGAAGAGCAAGGAACTTCAAAAGATCAAC 788
Db 255 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 274
QY 789 TGTGAACAACGTACAGCAAAATGGAACAATTAAGTGAAGAAATTAAGATTCACACTAGCCTA 848
Db 275 CysGluGlnArgThrGlyLysMetGluMetLysLysLysLysLysLysLysLysLys 294

395 HisGluAsnCysMetLeuLysGluLeuAlaMetLeuLysGluLeuAlaThrLeu 414
1209 AAACACCAATACAGGAAAGGAAATAAATCTTTGAGGACATTAAGATTTTAAAGAA 1268
415 LysHisGlnTyrGlnGlnLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGlu 434
1269 AGAATGCTGAATTCAGATGACC 1292
435 LysAsnAlaGluLeuGlnMetThr 442

RESULT 10
US-09-389-681-181
; Sequence 181, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-389-681-181

Alignment Scores:
Pred. No.: 1,17e-182 Length: 432
Score: 2017.00 Matches: 412
Percent Similarity: 96.06% Conservative: 3
Best Local Similarity: 95.37% Mismatches: 13
Query Match: 59.27% Indels: 5
Gaps: 0
DB: 4

US-09-602-362E-15 (1-2030) x US-09-389-681-181 (1-432)

741 GATACAGTTCACTTTGTGAAGAGCAAGGAACTTCAAAAAGATCACTGTGAACAACT 800
1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20
801 ACAGGAAATGCAACAAATGAAAGAGTTTGTGTACTGAAAGAAAGAACTGTGAGAA 860
21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40
861 GCAAAAGAAATAAATACAGATTAGAGAACCAAAAGTTTAAATGGGAAACAGAGCTCTGC 920
41 AlaLysGluLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluLysCys 60
921 AGTGTGAGATTGACTTTAAACAGAGAGAGAGAGAGAAATGCCGATATATTAAT 980
61 SerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAlaAspIleLeuAsn 80
981 GAAAAATAGGGAAGAAATTAGGAAGATCGAAGAGCAGCATAGGAAAGATTAGAAGTG 1040
81 GluLysIleArgGluGluLeuGlyArgIleGluGluGlnHisArgLysGluLeuVal 100
1041 AAACAACAATTGAAACAGGCTCTCAGAAATACAGATATAGAAATGAGAGTTAGAAAGT 1100
101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGluLeuLysSerValGluSer 120
1101 AATTTGAATCAGTTTCTCACCTCATGAAATGAAATATCTCTTACATGAAATTCG 1160
121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
1161 ATGTTGAAAAGGAAATGCCATGCTTAAACATGGAATAGCCACACTGAAACCAACATAC 1220
141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160

QY 1221 CAGGAAAGGAAATAAATACTTTGAGGACATTAAGATTTTAAAGAAAGAAATGCTGAA 1280
Db 161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180
QY 1281 CTTGAGATGACCCCTAAACCTGAAAGAGGAATCACTAACTAAAGGGCATCTCAATATAGT 1340
Db 181 LeuGlnMetThrLeuLysLeuLysGluLysSerLeuThrLysArgAlaSerGlnTyrSer 200
QY 1341 GGGCAGCTTAAAGTTCTGATAGCTGAGAACACAAATGCTCACTTCTAAATGAAGGAAAA 1400
Db 201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220
QY 1401 CAAGACAAAGAAATCTAGAGGCGAGAAATTAATCAACCATCTCTAGCTGCTTCTGCT 1460
Db 221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240
QY 1461 GTACAAGACCATGATCAAAATTTGTGACATCAAGAAAAAGTCAAGAACCTGCTTCCACATT 1520
Db 241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260
QY 1521 GCAGGAGATGCTTCTTTTCCAAAGAAAAATGAATGTTGATGTAGTAGTACCGATATATA 1580
Db 261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThrIleTyrAs 280
QY 1581 CAATGAGGTGCTCCATCAACCACTTCTGAGCTCAAGGAAATCCANAAGCCTAAAAAT 1640
Db 280 AsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysI 300
QY 1641 TAATCTCAATATGACGAGATGCTTAAGAGAAAAATACATTGTTTTCAGGAACATGCAC 1700
Db 300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320
QY 1701 AAAGAGACCAACGCTGAAACACAGTGTCAATGAAGGAGCTGACACATGNTCAAACNG 1760
Db 320 InArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340
QY 1761 AACAAAGATNATGTCAACAAACACACTGANCAGCAGGAGTCTCTAGATCAGAAAAATTATTC 1820
Db 340 luGlnAspAsnValAsnLysHisThrGluGlnGlnGlnSerLeuAspGlnLysLeuPheG 360
QY 1821 AACTACAAAGCAAAATATGTGGCTTCAACAGCAATTAAGTTTCATGTCATGACATAANGAAGCT 1880
Db 360 InLeuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379
QY 1881 GACAAACAAACCAAGATAAACAAATTTGATNTCTTGAGAGGAAAAATGCN-CATCAT 1939
Db 380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399
QY 1940 CTTCTAAAGAGAAAAATGAGAGATATTNATACNATACCATTTTAAAAAACCCGTAT 1999
Db 400 LeuLeuLysGluLysAsnGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgI 419
QY 2000 ATTTCAATATGGAAGAAAAAANAANAANA 2027
Db 419 etyGlnTyrGlnLysGluLysAlaGlu 428

RESULT 11

US-09-620-405B-181
; Sequence 181, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20

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; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-620-405B-181

Alignment Scores:
Pred. No.: 1,17e-182 Length: 432
Score: 2017.00 Matches: 412
Percent Similarity: 96.06% Conservative: 3
Best Local Similarity: 95.37% Mismatches: 13
Query Match: 59.27% Indels: 5
DB: 4 Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-620-405B-181 (1-432)

QY 741 GATACAGTTTCATTTCTGTAAGAGCAAGCAAGCACTTCAAAAGATCAGTGTGAACAAGCT 800
Db 1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20
QY 801 ACAGGAAAAATGCAACAAATGAAAGAAAGCTTTTGTGTACTGAAAAAGAACTGTGCAGAA 860
Db 21 ThrGlyLysMetGluGlnMetLysLysPheCysValLeuLysLysLysLeuSerGlu 40
QY 861 GCAAAAGAAATAAATCACAGTTAGAGAACCAAAAAAGTTAAATGGGAAACAAGAGCTCTGC 920
Db 41 AlaLysGluLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLeuCys 60
QY 921 AGTGTGAGATTGACTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Db 61 SerValArgLeuThrLeuLeuGlnGluGluGluGluGluGluGluGluGluGluGluGlu 80
QY 981 GAAAAAATTAGGAGAGAAATPAGGAGAAATCGAAGACGACGACATAGGAAAGAGTTAGAGTG 1040
Db 81 GluLysLeuArgGluGluLeuGluArgGluGluGlnHisArgLysGluLeuGluVal 100
QY 1041 AACAACACACTGCAAGAGCTCTCAGATACAGATATAGATTTGAGAGCTAGAGAGT 1100
Db 101 LysGlnGlnLeuGlnAlaLeuArgGluGlnAspLeuGluLeuLysSerValGluSer 120
QY 1101 AATTGCAATCAGTTTCTCACACTCTAGAAATGAAATTTATCTTACATGAAATTTGC 1160
Db 121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
QY 1161 ATGTTGAAAAGAAATTCGCATGCTAAACTGGAAATAGCCACACTGAAACCAACATAC 1220
Db 141 MetLeuLysLysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyr 160
QY 1221 CAGGAAAAGAAAATAAATACITTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGAA 1280
Db 161 GlnGluLysGluAsnLysTyrPheGluAspLeuLysLeuLysGluLysAsnAlaGlu 180
QY 1281 CTCAGATGACCTTAAACTGAAAGAGAAATCAATTAACATAAAGGCGATCTCAATATAGT 1340
Db 181 LeuGlnMetThrLeuLysLysLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200
QY 1341 GGGCAGCTTAAAGTCTGTAGTGTAGAGACACAACTGCTCACTTCTAAATTTGAAGGAAAAA 1400
Db 201 GlyGlnLysValLeuLeuAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220
QY 1401 CAAGACAAAGAAATATAGAGGAGAAATTTGAATCACACCATCTAGACTGCTTCTGCT 1460
Db 221 GlnAspLysGluLeuGluAlaGluLeuGluSerHisHisProArgLeuAlaSerAla 240
QY 1461 GTACAGACCATGATCAATTTGTGACATCAAGAAAAGTCAAGAACCTGCTTTCCACATT 1520
Db 241 ValGlnAspHisGlnLeuValThrSerArgLysSerGlnGluProAlaPheHisIle 260
QY 1521 GCAGGAGATGCTTTGTTGCAAAAGAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
Db 261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280

; SEQUENCE 181, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yugui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-339-338-181

Alignment Scores:
Pred. No.: 1,17e-182 Length: 432
Score: 2017.00 Matches: 412
Percent Similarity: 96.06% Conservative: 3
Best Local Similarity: 95.37% Mismatches: 13
Query Match: 59.27% Indels: 5
DB: 4 Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-339-338-181 (1-432)

QY 741 GATACAGTTTCATTTCTGTAAGAGCAAGCAAGCACTTCAAAAGATCAGTGTGAACAAGCT 800
Db 1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20
QY 801 ACAGGAAAAATGCAACAAATGAAAGAAAGCTTTTGTGTACTGAAAAAGAACTGTGCAGAA 860
Db 21 ThrGlyLysMetGluGlnMetLysLysPheCysValLeuLysLysLysLeuSerGlu 40
QY 861 GCAAAAGAAATAAATCACAGTTAGAGAACCAAAAAAGTTAAATGGGAAACAAGAGCTCTGC 920
Db 41 AlaLysGluLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLeuCys 60
QY 921 AGTGTGAGATTGACTTAAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Db 61 SerValArgLeuThrLeuLeuGlnGluGluGluGluGluGluGluGluGluGluGluGlu 80
QY 981 GAAAAAATTAGGAGAGAAATPAGGAGAAATCGAAGACGACGACATAGGAAAGAGTTAGAGTG 1040
Db 81 GluLysLeuArgGluGluLeuGluArgGluGluGlnHisArgLysGluLeuGluVal 100
QY 1041 AACAACACACTGCAAGAGCTCTCAGATACAGATATAGATTTGAGAGCTAGAGAGT 1100
Db 101 LysGlnGlnLeuGlnAlaLeuArgGluGlnAspLeuGluLeuLysSerValGluSer 120
QY 1101 AATTGCAATCAGTTTCTCACACTCTAGAAATGAAATTTATCTTACATGAAATTTGC 1160
Db 121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
QY 1161 ATGTTGAAAAGAAATTCGCATGCTAAACTGGAAATAGCCACACTGAAACCAACATAC 1220
Db 141 MetLeuLysLysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyr 160
QY 1221 CAGGAAAAGAAAATAAATACITTTGAGGACATTAAGATTTTAAAGAAAAGAAATGCTGAA 1280
Db 161 GlnGluLysGluAsnLysTyrPheGluAspLeuLysLeuLysGluLysAsnAlaGlu 180
QY 1281 CTCAGATGACCTTAAACTGAAAGAGAAATCAATTAACATAAAGGCGATCTCAATATAGT 1340
Db 181 LeuGlnMetThrLeuLysLysLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200
QY 1341 GGGCAGCTTAAAGTCTGTAGTGTAGAGACACAACTGCTCACTTCTAAATTTGAAGGAAAAA 1400
Db 201 GlyGlnLysValLeuLeuAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220
QY 1401 CAAGACAAAGAAATATAGAGGAGAAATTTGAATCACACCATCTAGACTGCTTCTGCT 1460
Db 221 GlnAspLysGluLeuGluAlaGluLeuGluSerHisHisProArgLeuAlaSerAla 240
QY 1461 GTACAGACCATGATCAATTTGTGACATCAAGAAAAGTCAAGAACCTGCTTTCCACATT 1520
Db 241 ValGlnAspHisGlnLeuValThrSerArgLysSerGlnGluProAlaPheHisIle 260
QY 1521 GCAGGAGATGCTTTGTTGCAAAAGAAAATGAATGTTGATGTGAGTAGTACCGATATATAA 1580
Db 261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280
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861 GCAAAAGAAATTAATACAGTGTAGACACCAAAAGTTAAATGGGAACAAGCTCTGC 920
Db 41 AlaLysGluLeuLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluCys 60
QY 921 AGTGTGAGATTGACCTTTAAACCAAGAAGAAGAGAAATGCCGATATTAAT 980
Db 61 SerValArgLeuThrLeuAsnGlnGluGluLysArgArgAsnAlaAspLeuAsn 80
QY 981 GAAAAANTAGGAAGAAATAGGAAGATCGAAGACGACATAGAAAGCTTACAAGT 1040
Db 81 GluLysLeuArgGluGluGluGlyArgGluGluGlnHisArgGlyGluGluVal 100
QY 1041 AAACAACAACCTTGAACAGCTCTCAGATACAGATATAGAAATTCGAAGTGTGAAGT 1100
Db 101 LysGlnGlnLeuGluGlnAlaLeuArgGlnGlnAspLeuGluLysSerValGluSer 120
QY 1101 AATTTGAATCAGTTCACACTCATGAATGAATGAATATCTCTTACATGAATTC 1160
Db 121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
QY 1161 ATGTTGAAAAGAAATTCCTCATGCTTAAACTGGAATAGCCACACTGAAACCAATAC 1220
Db 141 MetLeuLysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyr 160
QY 1221 CAGGAAACGAAATTAATACCTTGAAGACATTAATTTAAAGAAAGAAATCCTGAA 1280
Db 161 GlnGluLysGluAsnLysTyrPheGluAspLysLeuLysLeuLysGluLysAsnAlaGlu 180
QY 1281 CTTGAGATCAGCTTAACTGAAAGAGGAATCATTAACCTAAAGGCTCTCAATATAGT 1340
Db 181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200
QY 1341 GGCAGCTTAAAGTTCTGTAGCTGAGACACAATGCTCACTTCTAAATGAAGAAATA 1400
Db 201 GlyGlnLeuLysValLeuLeuAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220
QY 1401 CAGACAAAGAAATACAGGACGAGAAATGATCACACCATCCTAGCTGCTCTGCT 1460
Db 221 GlnAspLysGluLeuGluGluAlaGluLeuGluSerHisHisProArgLeuAlaSerAla 240
QY 1461 GTACAAGACCATGATCAAAATGTCATCAAGCTCAAGGAAATCAAGAACTGCTTCCACAT 1520
Db 241 ValGlnAspHisAspGlnLeuValThrSerArgLysSerGlnGluProAlaPheHisLe 260
QY 1521 GCAGGAGATGCTTTGTCAAAGAAATGAATGTTGATGTGAGTAGTACCATATATAA 1580
Db 261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerThrIleTyrAs 280
QY 1581 CAATGAGTGCTCCATCAACCACTTCTCAAGCTCAAGGAAATCCANAAGCTTAAAT 1640
Db 280 HisGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysAl 300
QY 1641 TAATCTCAATATGACGAGATGCTCTAAGAGAAATATCATTTGGTTTCAGGAACATGAC 1700
Db 300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSerGluHisAlaG 320
QY 1701 AAAGACCAACGTCGTAAGACACAGTGTCAATGAAGGAACTGAACACATGTTTCAAAACG 1760
Db 320 LysArgGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340
QY 1761 AACCAAGATNATGGAACAAACACATGANCAGCAGGAGTCTCTAGATCAGAATATTTC 1820
Db 340 LuGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360
QY 1821 AACTACAAGCAAAATATGTGCTTCAACAGCAATTAGTTCATGACACATAANGAAAGCT 1880
Db 360 LysGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHisLysLysAla 379
QY 1881 GACACAAAGCAAGATAACAATGATNTTCAATTTCTTTCAGAGGAAATGNC-CATCAT 1939
Db 380 AspAsnLysSerLysIleThrIleAspLysPheLeuGluArgLysMetGlnHisHis 399
QY 1940 CTTCTTAAAGAGAAATAGGAGATATTNTTATACNATAACCATTTAAAGAAACCCGTAT 1999

Db 400 LeuLeuLysGluLysAsnGluGluPheAsnTyrAsnAsnHisLeuLysAsn-ArgI 419
QY 2000 ATTTCAATATGGAAGAAAAAANAANA 2027
Db 419 eTyrGlnTyrGluLysGluLysAlaGlu 428
RESULT 13
US-09-433-826B-181
; Sequence 181, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47004
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-433-826B-181
Alignment Scores:
Pred. No.: 1,17e-182 Length: 432
Score: 2017.00 Matches: 412
Percent Similarity: 96.06% Conservative: 3
Best Local Similarity: 95.37% Mismatches: 13
Query Match: 59.27% Indels: 5
DB: 4 Gaps: 0
US-09-602-362E-15 (1-2030) x US-09-433-826B-181 (1-432)

QY 741 GATACAGTTTCATTTCTGTGAAGACGCAAGGAACTTCAAAAGATCACTGTGAACAAGT 800
Db 1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20
QY 801 ACAGAAATATGGAACAAATCAAAAGAGTTTGTCTACTGAAAAAGAACTCTCGAA 860
Db 21 ThrGlyLysMetGluGlnMetLysLysPheCysValLeuLysLysLysLeuSerGlu 40
QY 861 GCAAAAGAAATATAATCACAGTTAGAGAACCAAAAGCTTAAATCGGACCAAGAGCTCTGC 920
Db 41 AlaLysGluLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnGluCys 60
QY 921 ACTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAGAAATGCCGATATTAAT 980
Db 61 SerValArgLeuThrLeuAsnGlnGluGluGlyArgGluGlnHisArgLysGluLeuVal 80
QY 981 GAAAAAATTAGCGAAGAAATTAGGAAGAAATCGAAGACGACATAGCAAGAGTTAGAAGT 1040
Db 81 GluLysLeuArgGluGluLeuGluGlyArgGluGlnHisArgLysGluLeuVal 100
QY 1041 AAACAACAACCTTGAACAGCTCTCAGATACAGATATAGAAATTCGAAGTGTGAAGT 1100
Db 101 LysGlnGlnLeuGluGlnAlaLeuArgGlnGlnAspLeuGluLysSerValGluSer 120
QY 1101 AATTTGAATCAGTTCACACTCATGAATGAATGAATATCTCTTACATGAATTC 1160
Db 121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
QY 1161 ATGTTGAAAAGAAATTCCTCATGCTTAAACTGGAATAGCCACACTGAAACCAATAC 1220
Db 141 MetLeuLysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyr 160
QY 1221 CAGGAAAGGAAATATAATACCTTTCAGGACATTAAGATTTTAAAGAAAGAAAGTCTGAA 1280


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Db      280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysLeuLysI 300
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Db      300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320
QY      1701 AAAGAGACCAAGCTGAAACACACAGTGTCAATGAAGAAAGCTGAAACACATGNTCAAANCG 1760
Db      320 InArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340
QY      1761 AACAGATNATGTGAACAAACACATGANCACAGAGCTCTAGATCAGAAATATTTC 1820
Db      340 InGlnAspAsnValAsnLysHisThrGluGlnGlnGlnSerLeuAspGlnLysLeuPheG 360
QY      1821 AACTCAAAAGCAAAATATGTGGCTTCAACAGCAATATTAGTTCATGCACATAAAGAAAGCT 1880
Db      360 InLeuGlnSerLysAsnMetTyrLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379
QY      1881 GACAAACAAAGCAAGATTAATGCTTCAACAGCAATATTAGTTCATGCACATAAAGAAAGCT 1939
Db      380 AspAsnLysSerLysLysLeuThrLeuAspLysPheLeuGluArgLysMetGlnHisHis 399
QY      1940 CTTCTAAAAGAGAAATAGGAGATATTNNATTACNATAACCATTTAAAAAACCCTGAT 1999
Db      400 LeuLeuLysGluLysAsnGluGluLeuPheAsnTyrAsnAsnHisLeuLysAsn-ArgI 419

RESULT 15
US-09-285-480-181
; Sequence 181 Application US/09285480
; Patent No. 6590076
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C1
; CURRENT APPLICATION NUMBER: US/09/285,480
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-285-480-181

Alignment Scores:
Pred. No.: 1,178-182 Length: 432
Score: 2017.00 Matches: 412
Percent Similarity: 96.0% Conservative: 3
Best Local Similarity: 95.37% Mismatches: 13
Query Match: 59.27% Indels: 5
DB: 4 Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-285-480-181 (1-432)
QY      741 GATACAGTTCAATCTTGTGAAGAGCAAGGAACTTCAAAAGATCACTGTGAACAAAGCT 800
Db      1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20
QY      801 ACAGAAAAATGGAAACAATGAAGAAAGATTTGTGTACTGAAAGAAAGAACTGTCAAGAA 860
Db      21 ThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLysLysLeuSerGlu 40
QY      861 GCAAAGAAATATAATCAGTGTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGCG 920
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Db      41 AlalysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGluGlnLeuCys 60
QY      921 AGTGTGAGATTGACTTTTAAACCAAGAGAGAGAGAGAGAAATCGCGATATATTAAAT 980
Db      61 SerValArgLeuThrLeuAsnGlnGluGluGluLysArgArgAsnAlaAspIleLeuAsn 80
QY      981 GAAAAAATAGGGAAGAAATAGGAAGAATCGAAGAGCAGCATAGGAAGAGTTAGAAAGTG 1040
Db      81 GlulysIleArgGluLeuGluArgIleGluGluGlnHisArgLysGluLeuGluVal 100
QY      1041 AAACAACAACCTGAACAGGCTCTCAGNATACAGATATAGAAATGAAGAGTGTAGAAAGT 1100
Db      101 LysGlnGlnLeuGluGlnAlaLeuArgIleGlnAspIleGlnLeuLysSerValGluSer 120
QY      1101 AATTGAATCAGGTTTCTCACACTCATGAAAAATGAAAAATATTCTTACATGAAAAATTGC 1160
Db      121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
QY      1161 ATGTTGAAAAAGAAATGCGATGCTTAAACTGGAATAGCCACACTGAAACCCAAATAC 1220
Db      141 MetLeuLysLysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyr 160
QY      1221 CAGGAAAAGGAAAATAAATACTTTGAGGACATTAAGATTTTAAAGAAAAAGAAATGCTGAA 1280
Db      161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180
QY      1281 CTCGAGATGACCTTAAACTGAAAGAGGAATCATTAACATAAAGGGCATCTCAATATAGT 1340
Db      181 LeuGlnMetThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSer 200
QY      1341 GGGCAGCTTAAAGTTCTGATAGCTGAGACACAACTGCTCACTTCTAAATTAAGAGGAAAAA 1400
Db      201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLys 220
QY      1401 CAACACAAGAAATACTAGAGGAGAAATTAATGAATCAACACATCTAGACTGGCTTCTGCT 1460
Db      221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAla 240
QY      1461 GTACAGACCATCATCAAAATTTGTGACATCAAGAAAANGTCAGAAAGCTGTTTCCACATT 1520
Db      241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260
QY      1521 GCAGGAGATCTTGTGTTTCAAGAAAAATGAATGTTGATGTGAGTAGTAGCCGATATATAA 1580
Db      261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280
QY      1581 CAATGAGTCTCCATCAACACCATCTTCTGAAGCTCAAGAAATCCANAGCCTCAAAAT 1640
Db      280 nAsnGluValLeuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysI 300
QY      1641 TAATCTCAATATTGACAGGAGATGCTCTTAAGAGAAAAATACATTTGGTTTCAGGAACATGCAC 1700
Db      300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320
QY      1701 AAAGAGACCAAGCTGAAACACACAGTGTCAAATGAAGAAAGCTGAACACATGNTCAAANCG 1760
Db      320 InArgAspGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340
QY      1761 AACAGATNATGTGAACAAACACACATGANCACAGAGCTCTAGATCAGAAATATTTC 1820
Db      340 InGlnAspAsnValAsnLysHisThrGluGlnGlnGlnSerLeuAspGlnLysLeuPheG 360
QY      1821 AACTCAAAAGCAAAATATGTGGCTTCAACAGCAATATTAGTTCATGCACATAAAGAAAGCT 1880
Db      360 InLeuGlnSerLysAsnMetTyrLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379
QY      1881 GACAAACAAAGCAAGATTAATGCTTCAACAGCAATATTAGTTCATGCACATAAAGAAAGCT 1939
Db      380 AspAsnLysSerLysLysLeuThrLeuAspLysPheLeuGluArgLysMetGlnHisHis 399
QY      1940 CTTCTAAAAGAGAAATAGGAGATATTNNATTACNATAACCATTTAAAAAACCCTGAT 1999
Db      400 LeuLeuLysGluLysAsnGluGluLeuPheAsnTyrAsnAsnHisLeuLysAsn-ArgI 419
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QY 2000 ATTTCATATGGAAGAAAAAANAANA 2027
Db 419 eTyrGlnTyGluLysGluLysAlaGlu 428

RESULT 16

US-09-834-759-181
; Sequence 181, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 181
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-834-759-181

Alignment Scores:
Pred. No.: 1,170-182 Length: 432
Score: 2017.00 Matches: 412
Percent Similarity: 96.06% Conservative: 3
Best Local Similarity: 95.37% Mismatches: 13
Query Match: 59.27% Indels: 5
DB: 4 Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-834-759-181 (1-432)

QY 741 GATACATCTTCTTGTGAAGAGCAAGGAACTTCAAAAGATCATCTGCAACAGCT 800
Db 1 AspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHisCysGluGlnArg 20
QY 801 ACAGGAAATGCAACAATGAAAGAACTTGTGTACTGAAAGAACTGTGCAAA 860
Db 21 ThrGlyLeuMetGluGlnMetLysLysPheCysValLeuLysLysLeuSerGlu 40
QY 861 GCAAAAGAAATAAATACACAGTTAGAGAACCAAAAGTTAAATGGGAACAGAGCTCTGC 920
Db 41 AlaLysGluLeuLysSerGlnLeuGluLysValLysTrpGluGlnGluLeuCys 60
QY 921 AGTGTGAGATTGACTTAAACCAAGAGAGAGAGAGAGAAATCCCGATATTAAT 980
Db 61 SerValArgLeuThrLeuAsnGlnGluGluLysArgAsnAlaAspLeuLeuAsn 80
QY 981 GAAAAAATAGGGAAGAAATAGGAAGAAATCGAAGAGCAGCAGTAAAGTTAGAAAGTG 1040
Db 81 GluLysLeuArgGluGluLeuGlyArgGluGluGlnHisArgLysGluLeuGluVal 100
QY 1041 AACAACAATCTGAAAGCTCTCAGAAATACAGATATAGAAATGAGAGTGTAGAAAGT 1100
Db 101 LysGlnGlnLeuGluGlnAlaLeuArgGluGlnAspGluLeuLysSerValGluSer 120
QY 1101 AATTGCAATCAGTTCTCACATCTATGAAATGAAATATCTCTTACATGAAATATGTC 1160
Db 121 AsnLeuAsnGlnValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCys 140
QY 1161 ATGTTGAAAGAAATATGCGATCTTAAACTGGAATAGCCACATGAAACACCAATAC 1220
Db 141 MetLeuLysLysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyr 160
QY 1221 CAGGAAAGGAAATAAATATCTTTGAGCAGCATTAAGATTTTAAAGAAAAAGAAATGCTGAA 1280

Db 161 GlnGluLysGluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGlu 180
QY 1281 CTTTCAGATGACCTTAAACCTGAAAGAGGAATCAATTAATAAGGGCATCTCAATATAGT 1340
Db 181 LeuGlnMetThrLeuLysLysLeuLysGluLysSerLeuThrLysArgAlaSerGlnTyrSer 200
QY 1341 GGGCAGCTTAAAGTTCTGTATAGCTGAGACACAAATCTCTTAAATGTAAGGAAAA 1400
Db 201 GlyGlnLeuLysValLeuIleAlaGluAsnThrMetLeuThrSerLysLysLysGluLys 220
QY 1401 CAAGACAAGAAATACTAGAGGCAGAAATGAATCAACATCTAGCTAGCTGGCTTCTGCT 1460
Db 221 GlnAspLysGluIleLeuGluAlaGluIleGluSerHisProArgLeuAlaSerAla 240
QY 1461 GTACAGACCATGATCAAAATTTGTACATCAAGAAAAAGTCAAGAACTCTCTTCCCAT 1520
Db 241 ValGlnAspHisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIle 260
QY 1521 GCAGGATGCTTGTTCGCAAGAAATCAATGTTGATGTAGTAGTACCGATATATAA 1580
Db 261 AlaGlyAspAlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAs 280
QY 1581 CAATGAGTCTCATCAACCACTTCTTGAAGCTCAAGGAAATCCANAAGCCTTAAAT 1640
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Db 300 eAsnLeuAsnTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaG 320
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Db 320 LnaArgGlnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnG 340
QY 1761 AACAGATNATGTGAACAAACACACATGANCAGCAGGAGTCTTAGATCAGAAATTTATTC 1820
Db 340 LuGlnAspAsnValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheG 360
QY 1821 AACTTACAACCAAAATATCTGCTTCAACAGCAATTAGTTTCATGCACATTAAGAAAGCT 1880
Db 360 LnuGlnSerLysAsnMetTrpLeuGlnGlnGlnLeuValHisAlaHis-LysLysAla 379
QY 1881 GACAACAAAAGCAAGATAACAATTTGATTTTTCATTTCTTGAGAGGAAATGCN-CATCAT 1939
Db 380 AspAsnLysSerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHis 399
QY 1940 CTTCTTAAAGAGAAATAGAGAGATTTTNNATACNATAACCATTTAAAAACCCGTAT 1999
Db 400 LeuLeuLysGluLysAsnGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIle 419
QY 2000 ATTTCATATGGAAGAAAAAANAANA 2027
Db 419 eTyrGlnTyGluLysGluLysAlaGlu 428

RESULT 17

US-09-620-405B-469
; Sequence 469, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 469
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(650)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-620-405B-469

Alignment Scores:
Pred. No.: 7,11e-143 Length: 650
Score: 1597.50 Matches: 321
Percent Similarity: 83.42% Conservatives: 1
Best Local Similarity: 83.16% Mismatches: 2
Query Match: 46.94% Indels: 62
DB: 4 Gaps: 1

US-09-602-362E-15 (1-2030) x US-09-620-405B-469 (1-650)

QY 9 GTTAAAGATGGTCTCTGAGGCTAACTCGGGAATGAAGTTCTATTCCAACTAAAGCC 68
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QY 69 TTAGATTGATGCATGCAAACTTTCAAGCAGAGCCTCCGAGAAGCCATCTGCCTTC 128
Db 347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 366
QY 129 GAGCTGCGAATGAATGCAAAAGTCTGTTCAAATAAAGCCTTGAATTCGAAGATGAA 188
Db 367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386
QY 189 CAACATTGAGCAGATGAGTATCCCATCAGATCCAAACAAAGAGCTATGAAGAA 248
Db 387 GlnThrLeuArgAlaAspGluIleuProSerGluSerLysGlnLysAspPyrGluGlu 406
QY 249 AGTCTTGGGATCTTGAGAGTCTCTGTGAGAGTGTTCACAGAAGGATGTGTGTTACCC 308
Db 407 SerSerTrpAspSerGluSerLeuGluGlnThrValSerGlnLysAspValCysLeuPro 426
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QY 369 AATGATGGTTTCTGAAGGCTCCCTGCAGATGAAAGTTTCTATTCCAACTAAAGCCCTTA 428
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QY 429 GAATTGATGCATGCAAACTTTCAAGCAGAGCCTCCGAGAAGCCATCTGCCTTCGAG 488
Db 467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486
QY 489 CCGTCATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGAATTCGAAGATGAACAA 548
Db 487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506
QY 549 ACATTGAGCAGATCAGATGTTCCTTCAGAAATCAAAACAAAGAGGTTCAAGAAAT 608
Db 507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 526
QY 609 TCTTGGGATCTCAGAGTCTCCGTGAGAGTGTTCACAGAGGATGTGTGTCACCCAG 668
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QY 669 GGTACACATCAAAAGAAATGATATAAATAGTGGAAATTAGAAGATTCAACTAGCCCTA 728
Db 547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluLysSerThrSerLeu 566
QY 729 TCAAAATCTTGATACAGTTCATCTGTGTGAAGCAGAGGAACTTCAAAAGATCAC 788
Db 567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586
QY 789 TGTGAACACGTACAGGAAAAATGCAACAAATGCAAAAGAAAGTGTGTGTACTGAAAAAG 848
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Db 587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606
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Db 607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGlnAsnGlnLysValLysTrpGlu 626
QY 909 CAAGAGCTCTCAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAAATGCC 968
Db 627 GlnGluLeuCysSerVal----- 632
QY 969 GATATATTAATGAAAAAATAGGAGAGATTAGGAAGATCGAAGAGCAGCATAGGAAA 1028
Db 632 ----- 632
QY 1029 GAGTTAGAGTGAACAACTTGAACAGGCTCTCAGATACAGATATAGAAATGAAG 1088
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QY 1149 CATGAAATTCGATGT 1164
Db 645 rMetLysIleAlaCys 650

RESULT 18
US-09-433-826B-469
; Sequence 469, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.47004
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (310)
; NAME/KEY: Xaa = Any Amino Acid<221> unsure
; LOCATION: (429)
; NAME/KEY: Xaa = Any Amino Acid<221> unsure
; LOCATION: (522)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-433-826B-469

Alignment Scores:
Pred. No.: 7,11e-143 Length: 650
Score: 1597.50 Matches: 321
Percent Similarity: 83.42% Conservatives: 1
Best Local Similarity: 83.16% Mismatches: 2
Query Match: 46.94% Indels: 62
DB: 4 Gaps: 1

US-09-602-362E-15 (1-2030) x US-09-433-826B-469 (1-650)

QY 9 GTTAAAGATGGTCTCTGAGGCTAACTCGGGAATGAAGTTCTATTCCAACTAAAGCC 68
Db 327 VallyAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346
QY 69 TTAGATTGATGCATGCAAACTTTCAAGCAGAGCCTCCGAGAAGCCATCTGCCTTC 128
Db 347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 366
QY 129 GAGCTGCGAATGAATGCAAAAGTCTGTTCAAATAAAGCCTTGAATTCGAAGATGAA 188
Db 367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386
QY 189 CAACATTGAGCAGATGAGTATCCCATCAGATCCAAACAAAGAGCTATGAAGAA 248
Db 387 GlnThrLeuArgAlaAspGluIleuProSerGluSerLysGlnLysAspPyrGluGlu 406
QY 249 AGTCTTGGGATCTTGAGAGTCTCTGTGAGAGTGTTCACAGAAGGATGTGTGTTACCC 308
Db 407 SerSerTrpAspSerGluSerLeuGluGlnThrValSerGlnLysAspValCysLeuPro 426
QY 309 AAGGTACACATCAAAAGAATAGATAAATAATGAATAATGAAGATTCCTGAT 368
Db 427 LysAla***HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluGluSerProAsp 446
QY 369 AATGATGGTTTCTGAAGGCTCCCTGCAGATGAAAGTTTCTATTCCAACTAAAGCCCTTA 428
Db 447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466
QY 429 GAATTGATGCATGCAAACTTTCAAGCAGAGCCTCCGAGAAGCCATCTGCCTTCGAG 488
Db 467 GluLeuMetAspMetGlnThrPheLysAlaGluProProGluLysProSerAlaPheGlu 486
QY 489 CCGTCATTGAATGCAAAAGTCTGTTCAAATAAAGCCTTGAATTCGAAGATGAACAA 548
Db 487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506
QY 549 ACATTGAGCAGATCAGATGTTCCTTCAGAAATCAAAACAAAGAGGTTCAAGAAAT 608
Db 507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 526
QY 609 TCTTGGGATCTCAGAGTCTCCGTGAGAGTGTTCACAGAGGATGTGTGTCACCCAG 668
Db 527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546
QY 669 GGTACACATCAAAAGAAATGATATAAATAGTGGAAATTAGAAGATTCAACTAGCCCTA 728
Db 547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluLysSerThrSerLeu 566
QY 729 TCAAAATCTTGATACAGTTCATCTGTGTGAAGCAGAGGAACTTCAAAAGATCAC 788
Db 567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586
QY 789 TGTGAACACGTACAGGAAAAATGCAACAAATGCAAAAGAAAGTGTGTGTACTGAAAAAG 848
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Db 347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 366
QY 129 GAGCTGCGCATTAAGATGAAAGAGTCTGTTCCAAATTAAGCCTTGGAAATGAAGATGAA 188
Db 367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386
QY 189 CAAACATTGAGACAGACATGAGTACTCCCATCAGATCCAAACAAAGAGACTATCAAGAA 248
Db 387 GlnThrLeuArgAlaAspGluLeuLeuProSerGluSerLysGlnLysAspTyrGluGlu 406
QY 249 AGTTCTTGGAATCTCAGAGTCTCTGAGACTGTTTTCAGAAAGAGTGTGTTTACCC 308
Db 407 SerSerTrpAspSerGluSerLysGlnThrValSerGlnLysAspValCysLeuPro 426
QY 309 AAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATGAAGAGTCTCTGAT 368
Db 427 LysAla**HisGlnLysGluLeuAspLysIleAsnGlyLysLeuGluGluSerProAsp 446
QY 369 AATGATGTTTCTGAGGCTCCCTGCAGAAATCAAAAGTTTCTATTCCAACTAAAGCCTTA 428
Db 447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466
QY 429 GAATTCATGACATGCAAACTTCAAGCAGAGCCTCCCGAAGCCATCGCTTCGAG 488
Db 467 GluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPheGlu 486
QY 489 CTTGCCATTGAATCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATGAAGATGAACAA 548
Db 487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLysAsnGluGln 506
QY 549 ACATTGAGACAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTCAGAAAT 608
Db 507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys**ValGluGluAsn 526
QY 609 TCTTGGAATCTCAGAGTCTCCGTCAGACTGTTTCACAGAGAGTGTGTGTACCCCAAG 668
Db 527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546
QY 669 GTTACATCAAAAGAAATGATAAAATAAGTGGAAATTAAGAGATCAACTGAGCCTTA 728
Db 547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566
QY 729 TCAGAAATCTTGATCAGTCTCATCTCTGTAAGAGCAAGGAACTTCCAAAGATCAC 788
Db 567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586
QY 789 TGTGAACACGTACAGGAAATGGAACAAATGAAAGAAAGTTTGTGTACTGAAAGAA 848
Db 587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysIys 606
QY 849 ARACTTCAGACCAAGAAATTAATCAATCAGAGTACAGACCAAAAGTAAATGGGAA 908
Db 607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626
QY 909 CAAGAGCTCTGCAAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAAATGCC 968
Db 627 GlnGluLeuCysSerVal 632
QY 969 GATATATTAAATGAAAAATTAGGAGAAATTAGGAGAAATCGAAGACGAGCATAGGAA 1028
Db 632 632
QY 1029 GAGTTAGAGTGAACAACTTGAACAGGCTCTCAGAAATCAAGATATAGATTGAAG 1088
Db 632 632
QY 1089 AGTGTAAGAAATTAATTTGAATCAAGTTTCTCACATCTCATGAAATGAAATTAATCTCTTA 1148
Db 633 633
QY 1149 CATGAAATTTGCATGT 1164

Db 645 rMetLysIleAlaCys 650
RESULT 19
US-09-604-287A-469
; Sequence 469, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604, 287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (310)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: unsure
; LOCATION: (429)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: unsure
; LOCATION: (522)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-604-287A-469
Alignment Scores:
Pred No.: 7,11e-143 Length: 650
Score: 1597.50 Matches: 321
Percent Similarity: 83.42% Conservat: 1
Best Local Similarity: 83.16% Mismatches: 2
Query Match: 46.94% Indels: 62
DB: 4 Gaps: 1
US-09-602-362E-15 (1-2030) x US-09-604-287A-469 (1-650)
QY 9 GTTAAAGATGCTTCTGAAAGGCTAACTCGGAATGAAGTTTCTATTCCAACTAAGCC 68
Db 327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346
QY 69 TTGAATTTGATGACATGCAAACTTTCAAAGCAGAGCCTCCCGAAGCCATCTGCCTTC 128
Db 347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 366
QY 129 GAGCTGCCATTGAATGCAAAAGTCTGTTCCAAATAAAGCCTTGAATGAAGATGAA 188
Db 367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLysAsnGlu 386
QY 189 CAAACATTGAGACAGATGAGTACTCCCATCAGAAATCCAAACAAAGAGACTATGAAGAA 248
Db 387 GlnThrLeuArgAlaAspGluLeuLeuProSerGluSerLysGlnLysAspTyrGluGlu 406
QY 249 AGTTCTTGGAATCTCAGAGTCTCTGAGACTGTTTTCAGAAAGAGTGTGTTTACCC 308
Db 407 SerSerTrpAspSerGluSerLysGlnThrValSerGlnLysAspValCysLeuPro 426
QY 309 AAGGCTACACATCAAAAGAAATAGATAAAATAAATGGAATAATGAAGAGTCTCTGAT 368
Db 427 LysAla**HisGlnLysGluLeuAspLysIleAsnGlyLysLeuGluGluSerProAsp 446
QY 369 AATGATGTTTCTGAGGCTCCCTGCAGAAATCAAAAGTTTCTATTCCAACTAAAGCCTTA 428
Db 447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466

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QY 429 GAATTGATGACATCAAACTTCCAAAGCAGAGCTCCGAGAGCCATCTGCCTTCGAG 488
Db 467 GluLeuMetAspMetGlnThrPhelysAlaGluProGluProGluLysProSerAlaPheGlu 486
QY 489 CTGTCATTGAAATCCAAAGTCTGTTCAATAAAGCTTGGAAATCAAGAATCAACAA 548
Db 487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506
QY 549 ACATTGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGAAAT 608
Db 507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys**ValGluGluAsn 526
QY 609 TCTTGGGATTCGACAGTCTCGTGCAGACTGTTTCACAGAAGGATGTTGTGTACCCCAAG 668
Db 527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546
QY 669 GCTACACATCAAAAGAAATGGAATAAAGTGAAGAAATAGAACATTAAGAGCTTA 728
Db 547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566
QY 729 TCAGAAATCTTGATACAGTTCATCTTGTGAAGAGCAAGGAACTTCAAAAGATCAC 788
Db 567 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 586
QY 789 TGTGAACAACGTACAGGAAATGGAACAAATGAAAGAAAGATTTTGTGTACTGAAAGAG 848
Db 587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 606
QY 849 AACTGTGAGAGCAAGAAAGAAATAAATCAAGTTAGAGAACCAAAAGTTAAATGGAA 908
Db 607 LysLeuSerGluAlaLysGluLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626
QY 909 CAAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAAATGCC 968
Db 627 GlnGluLeuCysSerVal----- 632
QY 969 GATATATTAAATGAAAAATTAGGAGAGAAATAGGAAGATCGAAGACAGCATAGGAAA 1028
Db 632 ----- 632
QY 1029 GAGTTAGAGTGAACAACTTGAACAGGCTCTCAGATACAGATATAGATTAAGAG 1088
Db 632 ----- 632
QY 1089 AGTGTAGAAAGTAATTGAATCAGTCTTCTCACACTCATGAAATGAAATTAATCTCTTA 1148
Db 633 -----Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 645
QY 1149 CATGAAATTCATGT 1164
Db 645 rMetLysIleAlaCys 650

RESULT 20
US-09-834-759-469
; Sequence 469, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 469
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LENGTH: 650
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (310)
OTHER INFORMATION: Xaa = Any Amino Acid
NAME/KEY: unsure
LOCATION: (429)
OTHER INFORMATION: Xaa = Any Amino Acid
NAME/KEY: unsure
LOCATION: (522)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-834-759-469

Alignment Scores:
Pred. No.: 7,11e-143 Length: 650
Score: 1597.50 Matches: 321
Percent Similarity: 83.42% Conservative: 1
Best Local Similarity: 83.16% Mismatches: 2
Query Match: 46.94% Indels: 62
DB: 4 Gaps: 1
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US-09-602-362B-15 (1-2030) X US-09-834-759-469 (1-650)

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QY 9 GTTAAAGATGGTCTTCTGAAGGCTAACTCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
Db 327 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 346
QY 69 TTGAATTTGATGACATGCAAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTGCCTTC 128
Db 347 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 366
QY 129 GAGCTGCCATTCAAAATGCAAAAGTCTGTTCACAAATAAGCCCTTGAATGAAAGATGAA 188
Db 367 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 386
QY 189 CAAACATTTGAGACAGATGAGATCTCCCATCAGAAATCCAAACAAAGGCTATGAGAA 248
Db 387 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyGluGlu 406
QY 249 AGTCTTGGATCTCAGAGTCTCTGAGACTGTTTCACAGAGGATGTTGTGTACCC 308
Db 407 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 426
QY 309 AAGCTACACATCAAAAGAAATAGATAAAATAATAGAAATAGAAATAGAAAGTCTCTGAT 368
Db 427 LysAla**HisGlnLysGluIleAspLysIleAsnGlyLysLeuGluSerProAsp 446
QY 369 AATGATGGTCTTCTGAAGCTCCCTCCAGATGAAAGTTTCTATTCCAACTAAAGCTTA 428
Db 447 AsnAspGlyPheLeuLysAlaProCysArgMetLysValSerIleProThrLysAlaLeu 466
QY 429 GAATTGATGACATGCAAACTTTCAAGCAGAGCCCTCCGAGAGCCATCTGCCTTCGAG 488
Db 467 GluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPheGlu 486
QY 489 CTGTCATTGAAATGCAAAAGTCTGTTCAATAAAGCTTGGAAATGAAAGTGAACAA 548
Db 487 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 506
QY 549 ACATTGAGCAGATCAGATGTTCCCTTCAGAAATCAAAACAAAGAGGTTGAAGAAAT 608
Db 507 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys**ValGluGluAsn 526
QY 609 TCTTGGGATTCGAGACTCTCGTGCAGACTGTTTCACAGAAGGATGTTGTGTACCCCAAG 668
Db 527 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 546
QY 669 GCTACACATCAAAAGAAATGGAATAAAGTGAAGAAATAGAACATTAAGAGCTTA 728
Db 547 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 566
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QY 729 TCAAAATCTTGATACAGTTCATTCTTCTGTAAGAGCAAGGAACTTCAAAAGATCAC 788
Db 567 SerLysIleLeuAspThrValHisSerCysGluA-gAlaArgGluLeuGlnLysAspHis 586
QY 789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAGAAAGTCTTGTACTGAAAAAG 848
Db 587 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysPheCysValLeuLysLys 606
QY 849 AAATCTCAGAACCAAGAAATATAATCACAGTTAGAGAACCAAAAGTTAAATGGAA 908
Db 607 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 626
QY 909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAAATGCC 968
Db 627 GlnGluLeuCysSerVal----- 632
QY 969 GATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAGAAATCGAAGAGCAGCATAGGAAA 1028
Db 632 ----- 632
QY 1029 GAGTTAGAGTGAACAACAACACTTGAAACAGGCTCTCAGAAATACAAGATATAGAAATTGAAG 1088
Db 632 ----- 632
QY 1089 AGTTAGAAAGTAATTGAATCAGGTTCTCACACTCATGAAAAATGAAAAATTCCTTA 1148
Db 633 -----Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 645
QY 1149 CATGAAATTCATGT 1164
Db 645 rMetLysIleAlaCys 650
RESULT 21
US-09-620-405B-494
; Sequence 494, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 494
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1).....(743)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-620-405B-494
Alignment Scores:
Pred. No.: 7,44e-143 Length: 743
Score: 1597.50 Matches: 321
Percent Similarity: 83.42% Conservative: 1
Best Local Similarity: 83.16% Mismatches: 2
Query Match: 46.94% Indels: 62
DB: 4 Gaps: 1
US-09-602-362E-15 (1-2030) x US-09-620-405B-494 (1-743)
QY 9 GTTAAAGATGGTCTCTGAGGCTACTCGGAATGAAGTTCTATTCCAACTAAAGCC 68
Db 420 ValLysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleLeuProThrLysAla 439

QY 69 TTAGNATTGATGACATGCAAACTTTCAAGCAGAGAGCTCCGAGAGCCATCTGCCTTC 128
Db 440 LeuGluLeuMetAspMetGlnThrPheLysAlaGluProGluLysProSerAlaPhe 459
QY 129 GAGCTGCCATTGAAATGCAAAAGTCTGTTTCCAAATAAAGCCCTTGAATGGAATGAA 188
Db 460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479
QY 189 CAAACATTGAGACAGATGAGATCTCCCATCAGATCCAAACAAAGAGACATGAGAA 248
Db 480 GlnThrLeuArgAlaAspGluIleLeuProSerGluSerLysGlnLysAspTyGluGlu 499
QY 249 AGTCTTGGGATCTGAGAGTCTCTGTGAGACTGTGTTTCAAGAGGATGTGTGTTTACC 308
Db 500 SerSerTrpAspSerGluSerLeuCysGluThrValSerGlnLysAspValCysLeuPro 519
QY 309 AAGCTACACATCAAAAGAAATAGATATAAATAAGTGAATAATGAGAGTCTCTGAT 368
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QY 369 AATGATGCTTTCTGAGGCTCCCTGCAGATGAAAGTTTCTATTCCAACTAAAGCCTTA 428
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Db 580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 599
QY 549 ACATTGAGACAGATCAGATGTTTCCCTTCCAGATCAAAACAAAGAGGTTGAAAGAAAT 608
Db 600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619
QY 609 TCTTGGGATCTGAGAGTCTCCGTGAGAGTCTTTCACAGAGAGATGTGTGTACCCAG 668
Db 620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639
QY 669 GCTACACATCAAAAGAAATGGAATAAATGGAATAAATGGAATAAATGGAATAAATG 728
Db 640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659
QY 729 TCAAAATCTTGGATCAGTTCATTCTTGTGAAGAGCAAGGAACTTCAAAAGATCAC 788
Db 660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679
QY 789 TGTGAACAACGTACAGGAAAAATGGAACAAATGAAAGAAAGTCTTGTACTGAAAAAG 848
Db 680 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysPheCysValLeuLysLys 699
QY 849 AAATCTCAGAACCAAGAAATATAATCACAGTTAGAGAACCAAAAGTTAAATGGGAA 908
Db 700 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 719
QY 909 CAAGAGCTCTGCAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAAATGCC 968
Db 720 GlnGluLeuCysSerVal----- 725
QY 969 GATATATTAAATGAAAAAATTAGGGAAGAAATTAGGAGAAATCGAAGAGCAGCATAGGAAA 1028
Db 725 ----- 725
QY 1029 GAGTTAGAGTGAACAACAACACTTGAAACAGGCTCTCAGAAATACAAGATATAGAAATTGAAG 1088
Db 725 ----- 725
QY 1089 AGTTAGAAAGTAATTGAAATCAGGTTCTCACACTCATGAAAAATGAAAAATTCCTTA 1148
Db 726 -----Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 738

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QY 1149 CATGAAAATTGCATGT 1164
Db 738 rMetLysIleAlaCys 743

RESULT 22
US-09-834-759-494
; Sequence 494, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 494
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variant
; LOCATION: (1)...(743)
; OTHER INFORMATION: Xaa = Any amino acid
US-09-834-759-494

Alignment Scores:
Pred. No.: 7,44e-143 Length: 743
Score: 1597.50 Matches: 321
Percent Similarity: 83.42% Conservative: 1
Best Local Similarity: 83.16% Mismatches: 2
Query Match: 46.94% Indels: 62
DB: 4 Gaps: 1

US-09-602-362E-15 (1-2030) x US-09-834-759-494 (1-743)
QY 9 GTTAAGATGCTTCTGAGGCTAACTCGGAATGAAAGTTTCTATTCCAACTAAAGCC 68
Db 420 VallysAspGlyLeuLeuLysAlaAsnCysGlyMetLysValSerIleProThrLysAla 439
QY 69 TTAGATTTCATGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAAGCCATCTGCCCTTC 128
Db 440 LeuGluLeuMetAspMetGlnThrPhelLysAlaGluProProGluLysProSerIlePhe 459
QY 129 GAGCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGATCAA 188
Db 460 GluProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGlu 479
QY 189 CAAACATTGACAGCAGATGAGATCTCCCATCAGAAATCCAAACAAAGGACTATGAAGAA 248
Db 480 GlnThrLeuArgAlaAspGluLeuLeuProSerGluSerLysGlnLysAspPyrGluGlu 499
QY 249 AGTTCTGGCATCTGAGAGTCTCTGTGAGACTGTTTCCACAGAAGGATGTGTGTTACCC 308
Db 500 SerSerTrpAspSerGluSerLeuLysGluThrValSerGlnLysAspValCysLeuPro 519
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QY 429 GAATTGATGACATGCAAACTTTCAAAGCAGAGCCTCCGAGAAGCCATCTGCCCTCAG 488
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Db 560 GluLeuMetAspMetGlnThrPhelLysAlaGluProProGluLysProSerAlaPheGlu 579
QY 489 CCTGCCATTGAAATGCAAAAGTCTGTTCCAAATAAAGCCTTGGAAATTGAAGATGAACAA 548
Db 580 ProAlaIleGluMetGlnLysSerValProAsnLysAlaLeuGluLeuLysAsnGluGln 599
QY 549 ACATTGAGCAGCAGATCAGATGTTCCCTTCCAGATCAAAACAAAGAGAGGTTGAAGAAAT 608
Db 600 ThrLeuArgAlaAspGlnMetPheProSerGluSerLysGlnLys***ValGluGluAsn 619
QY 609 TCTTGGGATTTGAGAGTCTCCGTGAGACTGTTTCCACAGAAGGATGTGTGTACTCCCAAG 668
Db 620 SerTrpAspSerGluSerLeuArgGluThrValSerGlnLysAspValCysValProLys 639
QY 669 GCTACACATCAAAAGAAATGATATAAATAAGTGGAAAAATTAGAAATTCAACTAGCCTTA 728
Db 640 AlaThrHisGlnLysGluMetAspLysIleSerGlyLysLeuGluAspSerThrSerLeu 659
QY 729 TCAAAATCTTGGATACAGTTCATTCTTGTGAAAGAGCAAGGAACTTCAAAAAGATCAC 788
Db 660 SerLysIleLeuAspThrValHisSerCysGluArgAlaArgGluLeuGlnLysAspHis 679
QY 789 TGTGAACAACTACAGGAAAAATGGAACAAATGAAAAAGAGTTTCTGTACTGAAAAAG 848
Db 680 CysGluGlnArgThrGlyLysMetGluGlnMetLysLysLysPheCysValLeuLysLys 699
QY 849 AAAGTGTGAGAGCAAGCAAAAGAAATTAATACAGTTAGAGAACCAAAAGTAAATGCGAA 908
Db 700 LysLeuSerGluAlaLysGluIleLysSerGlnLeuGluAsnGlnLysValLysTrpGlu 719
QY 909 CAGAGCTCTGAGTGTGAGATTGACTTTAAACCAAGAGAGAGAGAGAGAGAAATGCC 968
Db 720 GlnGluLeuCysSerVal----- 725
QY 969 GATATATTAAATGAAAAAATTAGGAAGAAATTAGGAAGAAATCGAGAGCAGCATAGGAAA 1028
Db 725 ----- 725
QY 1029 GAGTTAGAGTGAACCAACAACTTTGAACAGGCTCTCAGAAATACAAGATATAGAAATTGAAG 1088
Db 725 ----- 725
QY 1089 AGTGTAGAAAGTAATTTGAATCAGGTTTCTCAGACTCATGAAATGAAATTTATCTCTTA 1148
Db 726 -----Arg-PheLeuThrLeuMetLysMetLysIleIleSerTy 738
QY 1149 CATGAAAATTGCATGT 1164
Db 738 rMetLysIleAlaCys 743

RESULT 23
US-09-620-405B-495
; Sequence 495, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 495
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-405B-495
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Db 69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88
QY 1350 AAAGTTCTGATAGCTGAGAACCAATGCTCACTTCTAAATGAGGAAACACAGACAAA 1409
Db 89 LysValLeuLeuAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY 1410 GAAATACTAGAGGACAGAAATGAATCAACACACCATCTAGAGCTGGCTTCTGCTCAAGAC 1469
Db 109 GluLeuLeuGluAlaGluLeuGluSerHisProArgLeuAlaSerAlaValGlnAsp 128
QY 1470 CATGATCAAAATGTCACACAGAAAGAAAGTCAAGAACTGCTTCCACATTCAGAGAGAT 1529
Db 129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY 1530 GCTTGTTTCCAAAGAAATGAATGTGATGTAGTAGTACGATATATAACAATGAGCT 1589
Db 149 AlaCysLeuGluArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVal 168
QY 1590 GTCCATCAACACACTTCTGAAGCTCAAGGAAATCCANAAGCCTAAATAATCTCAA 1649
Db 168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLysIleAsnLeuAs 188
QY 1650 TTATCAGAGAGATGCTTCAAGGAAATGAGGAACTGCAACATGTNTCAAANCGAACAGATN 1769
Db 208 InArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAsp 228
QY 1770 ATGTGACAAACACACTGAGGAGAGTCTAGATTCAGAGGAAATGCTTCCACATCTCTAAA 1948
Db 268 SerLysIleThrIleAspIleHisPheLeuGluAlaGlyMetGlnHisLeuLeuLys 287
QY 1949 GAGAAAAATGAGGAGATATTNATACNATACCATTTAAACCCCGTATATTTCAATA 2008
Db 288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307

; US-09-433-826B-176
; Sequence 176, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRN
; ORGANISM: Homo sapien
; US-09-433-826B-176
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Alignment Scores:
Pred. No.: 5.38e-124 Length: 317
Score: 1397.00 Matches: 288
Percent Similarity: 94.50% Conservative: 4
Best Local Similarity: 93.20% Mismatches: 13
Query Match: 41.05% Indels: 5
DB: 4 Gaps: 0

US-09-602-362B-15 (1-2030) x US-09-433-826B-176 (1-317)
QY 1110 CAGTTTCTCAGCTCATGATAAATGAAAAATATCTCTTACATGAAAAATTCATGTTGAAA 1169
Db 9 GluValSerHisThrHisGluAsnGluAsnTyrLeuLeuHisGluAsnCysMetLeuLys 28
QY 1170 AAGGAAATTCCTCATCTGATAAAGTGAATAGCCACACTGAAACACCAATACCCAGGAAAG 1229
Db 29 LysGluLeuAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48
QY 1230 GAAATATAATCTTTGAGGACATTAAAGATTTTAAAGAAAAAGAAATGCTGAACTTCAGATG 1289
Db 49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
QY 1290 ACCCTRAAACTGAAGAGGAATCATTAACCTAAAGGCGCATCTCAATATAGTGGCAGCTT 1349
Db 69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88
QY 1350 AAAGTTCTGATAGCTGAGAACACAAATGCTCAGCTTCTAAATTTGAAGGAAAAACAGACAAA 1409
Db 89 LysValLeuLeuAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY 1410 GAAATACTAGAGGACAGAAATGAAATGACACATCTAGAGCTTCTGCTGTCAGACAGAC 1469
Db 109 GluLeuLeuGluAlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAsp 128
QY 1470 CATCATCAAAATTTGACATCAAGAAAAAGTCAAGAACTGCTTTCACATTCAGAGAGAT 1529
Db 129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY 1530 GCTTGTTTCCAAAGAAATGAATGTGATGTAGTAGTACGATATATAACAATGAGCT 1589
Db 149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVal 168
QY 1590 GCTCCATCAACCACTTCTGAGCTCAAGGAAATCCANAAGCCTAAATAATTCATCTCAA 1649
Db 168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188
QY 1650 TTATCAGAGAGATGCTCTAAAGAAAAATACATTTGGTTTCAGGAAACATGCACAAAGAGAC 1709
Db 188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208
QY 1710 AACGTGAAACACAGTGTCAATGAGGAACTGAAACATGTNTCAAANCGAACAGATN 1769
Db 208 InArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAsp 228
QY 1770 ATGTGAAACAAACACACTGAGGAGAGTCTAGATTCAGAGGAAATGCTTCCACATCTAAA 1829
Db 228 snValAsnLysHisThrGluGlnGlnSerLeuAspGlnLysLeuPheGlnLeuGlns 248
QY 1830 GCAAAAAATATGCTGCTTCAACAGCAATAGTTCATGCACATTAANGAAAGCTCAACAAA 1889
Db 248 erLysAsnMetTrpLeuGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267
QY 1890 AGCAAGATAACAATTTGATNTTCTTCTTGGAGAGGAAATGCTN-CATCATCTCTTAAAA 1948
Db 268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisLeuLeuLys 287
QY 1949 GAGAAAAATGAGGAGATATTNATACNATACCATTTAAACCCCGTATATTTCAATA 2008
Db 288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307
QY 2009 TGGAAAAAANAANAANA 2027
Db 307 rGluLysGluLysAlaGlu 313

RESULT 28
US-09-433-826B-176
; Sequence 176, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRN
; ORGANISM: Homo sapien
; US-09-433-826B-176
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188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208
1710 AACGTGAAACACAGTGTCAAAATGAAGAGCTGAACACATGTNTCAAACGAAACAGATN 1769
208 InArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228
1770 ATGTGAACAAACACACAGTGTCAAAATGAAGAGCTGAACACATGTNTCAAACGAAAC 1829
228 snValAsnLysHisThrGluGlnGlnSerLeuAspGlnLysLeuPheGlnGlnGlnS 248
1830 GCAAAAATATGTGCTTCAACAGCAATAGTTCATGCACATAAAGAAAGCTGACACAAA 1889
248 erLysAsnMetTyrLeuGlnGlnGlnValHisAlaHis-LysLysAlaAspAsnLys 267
1890 AGCAAGATAACAATTGATNTTCATTTCTTGAGAGGAATGCG-CATCATCTTCTTAAA 1948
268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisHisLeuLeuLys 287
1949 GAGAAAATGAGGAGATATTTTATACNATAACCAATTTAAAAAACCCGTATATTTCAATA 2008
288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307
2009 TGGAAAAAANAANAANA 2027
307 rGluLysGluLysAlaGlu 313

RESULT 30
US-09-285-480-176
; Sequence 176, Application US/09285480
; Patent No. 8590076
; GENERAL INFORMATION:
; APPLICANT: Yuqui, Jjiang
; APPLICANT: Dillon, Jennifer L.
; APPLICANT: Xu, Jjiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C1
; CURRENT APPLICATION NUMBER: US/09/285,480
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-285-480-176

Alignment Scores:
Pred. No.: 5.38e-124 Length: 317
Score: 1397.00 Matches: 288
Percent Similarity: 94.50% Conservative: 4
Best Local Similarity: 93.20% Mismatches: 13
Query Match: 41.05% Indels: 5
DB: Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-604-287A-176 (1-317)
QY 1110 CAGTTTCTCACACTCATGAAATGAAATATCTCTTACATGAAATTCGATGTTGAAA 1169
DB 9 GluValSerHisThrHisGluAsnGluAsnTyrLeuHisGluAsnCysMetLeuLys 28
QY 1170 AAGGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1229
DB 29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLys 48
QY 1230 GAAATAAATCTTGTGAGGACATTAAGATTTTAAAAAGAAAGATGCTGAATTCAGATG 1289
DB 49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
QY 1290 ACCCTAAACTGGAAGAGGAATCATTAACATAAAGGCGATCTCAATATAGTGGCAGCTT 1349
DB 69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88

US-09-604-287A-176
; Sequence 176, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jjiang, Yugui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jjiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-604-287A-176

Alignment Scores:
Pred. No.: 5.38e-124 Length: 317
Score: 1397.00 Matches: 288
Percent Similarity: 94.50% Conservative: 4
Best Local Similarity: 93.20% Mismatches: 13
Query Match: 41.05% Indels: 5
DB: Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-604-287A-176 (1-317)
QY 1110 CAGTTTCTCACACTCATGAAATGAAATATCTCTTACATGAAATTCGATGTTGAAA 1169
DB 9 GluValSerHisThrHisGluAsnGluAsnTyrLeuHisGluAsnCysMetLeuLys 28
QY 1170 AAGGAAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1229
DB 29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGlnLys 48
QY 1230 GAAATAAATCTTGTGAGGACATTAAGATTTTAAAAAGAAAGATGCTGAATTCAGATG 1289
DB 49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
QY 1290 ACCCTAAACTGGAAGAGGAATCATTAACATAAAGGCGATCTCAATATAGTGGCAGCTT 1349
DB 69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88
QY 1350 AAGTTTCTGATAGTGAACACAAATGCTCCTTCTTAAATTTGAAGAAAAAACAAGACAAA 1409
DB 89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY 1410 GAATTAAGTACAGGAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1469
DB 109 GluIleLeuGluAlaGluIleGluSerHisThrLysArgAlaSerGlnTyrSerGlyGlnLeu 128
QY 1470 CATGATCAAAATTCGACATCAAGAAAGTCAAGAACCTGCTTTTCCACATTCAGGAGAT 1529
DB 129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY 1530 GCTTGTTCGAAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1589
DB 149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyrAsnAsnGluVa 168
QY 1590 GCTCCATCAACACTTCTTGAAGCTCAAGAAAGTCAAGAACCTGCTTTTCCACATTCAGGAGAT 1649
DB 168 IleHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188
QY 1650 TTATGAGAGAGATGCTCTAAGAGAAATATCATTTGTTTTCAGGAAACATGACAAAGAGACC 1709
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QY 1350 AAAGTTCTGATAGCTGAGACAAATGCTCACTTTTAAATTCAGGAAAAACACACAAA 1409
Db 89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY 1410 GAAATCTAGAGGCGAGAAATTCGAATCACACCACTCTAGACTGGCTTCTGCTGTACAAGAC 1469
Db 109 GluIleLeuGluAlaGluIleGluSerHisProArgLeuAlaSerAlaValGlnAsp 128
QY 1470 CATGATCAAAATGTGACATCAGAAAAGTCAAGAACTGTTTCCACATTCGAGGAGAT 1529
Db 129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY 1530 GCTTGTCTGCAAGAAAAATGAATCTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
Db 149 AlaCysLeuGlnArgLysMetAsnValAspValSerThr-IleTyrAsnAsnGluVal 168
QY 1590 GTCCATCAACCACTTCTGAAGCTCAAGAGAAATCCANAAGCTTAAATAATATCTCAA 1649
Db 168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188
QY 1650 TTATGCAGGAGATGCTCTAAGAGAAAATACATTTGCTTTCAGGAACATGCACAAAGAGACC 1709
Db 188 nIyZAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208
QY 1710 AACGTGAACACAGTGTCAAATGAAGAGAGCTGAACACATGTNTCAAANCGAACACAAA 1769
Db 208 InArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228
QY 1770 ATGTGAACAAACACATGNCAGCAGGAGTCTTAGATCAGAAATTTTCAACTACAAA 1829
Db 228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248
QY 1830 GCAAAAAATATGTGGTCTCAACAGCAATTAGTTTCATCGCACATAAAGAAAGCTGCACAAA 1889
Db 248 eRLysAsnMetTrpLeuGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267
QY 1890 ACCAAGATACAAATGTATNTTCATNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAA 1948
Db 268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisLeuLeuLys 287
QY 1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTTAAAAAACCCGTATATTTCAATA 2008
Db 288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307
QY 2009 TCGAAAAAANAANAANAANA 2027
Db 307 rGluLysGluLysAlaGlu 313
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RESULT 31

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US-09-834-759-176
; Sequence 176, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-834-759-176
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Alignment Scores:
Pred. No.: 5,38e-124 Length: 317
Score: 1397.00 Matches: 288
Percent Similarity: 94.50% Conservative: 4
Best Local Similarity: 93.20% Mismatches: 13
Query Match: 41.05% Indels: 5
DB: 0 Gaps: 0

US-09-602-362E-15 (1-2030) x US-09-834-759-176 (1-317)
QY 1110 CAGGTTTCTCACACTCATGAAAAATGAAAATTTACTCTTACATGAAAAATTCATGTTGAAA 1169
Db 9 GluValSerHisThrHisGluAsnGluAsnTyr-LeuLeuHisGluAsnCysMetLeuLys 28
QY 1170 AAGGAATTCCTGCTTAAACTGGAATAGCCACACTGNAACACCAATACCAAGGAAAAG 1229
Db 29 LysGluIleAlaMetLeuLysLeuGluIleAlaThrLeuLysHisGlnTyrGlnGluLys 48
QY 1230 GAAAAATAAATACTTTGAGGACATTAAAGATTTTAAAAAGAAAAGAAATGCTGAACCTTCAGATG 1289
Db 49 GluAsnLysTyrPheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
QY 1290 ACCCTAAACTGAAAGAGGAATCATTAACCTAAAGGCGCATCTCAATATAGTGGCGAGCTT 1349
Db 69 ThrLeuLysLeuLysGluGluSerLeuThrLysArgAlaSerGlnTyrSerGlyGlnLeu 88
QY 1350 AAAGTTCTGATAGCTGAGAACACAACTGCTCACTTTCTAAATTTGAAGGAAAAACAAAGACAAA 1409
Db 89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY 1410 GAAATCTAGAGGCGAGAAATTTGAATCACACCATCTCTAGACTGGCTTCTGCTGTACAAGAC 1469
Db 109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128
QY 1470 CATGATCAAAATTTGACATCAAGAAAAGTCAGAAACCTGCTTTCCACATTCGAGGAGAT 1529
Db 129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY 1530 GCTTGTCTGCAAGAAAAATGAATGTGTGATGTGAGTAGTACCGATATATAACAATGAGGT 1589
Db 149 AlaCysLeuGlnArgLysMetAsnValAspValSerThr-IleTyrAsnAsnGluVal 168
QY 1590 GCTCCATCAACCACTTCTGAAGCTCAAGGAATTCANAGCCTTAAATAATTTCTCAA 1649
Db 168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188
QY 1650 TTATGCAGGAGATGCTCTTAAGAGAAAATACATTTGGTCTTTCAGGAACATGCACAAAGAGACC 1709
Db 188 nTyrAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208
QY 1710 AAGGTGAACACAGTGTCAAATGAAGAGAGCTGAACACATGTNTCAAANCGAACACAGATN 1769
Db 208 InArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyrGlnAsnGluGlnAspA 228
QY 1770 ATGTGAACAAACACACTGANCAGCAGGAGTCTTAGATCAAGAAATTTTCAACTACAAA 1829
Db 228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248
QY 1830 GCAAAAAATATGTGGTCTCAACAGCAATTAGTTTCATGCACATAAAGAAAGCTGCACAAA 1889
Db 248 eRLysAsnMetTrpLeuGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267
QY 1890 ACCAAGATACAAATGTATNTTCATNTCTTGAGAGGAAAATGCN-CATCATCTTCTAAA 1948
Db 268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisLeuLeuLys 287
QY 1949 GAGAAAAATGAGGAGATATTTNATTACNATAACCATTTTAAAAAACCCGTATATTTCAATA 2008
Db 288 GluLysAsnGluGluIlePheAsnTyrAsnAsnHisLeuLysAsn-ArgIleTyrGlnTy 307
QY 2009 TCGAAAAAANAANAANAANA 2027
Db 307 rGluLysGluLysAlaGlu 313
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Db      307 rGluLysGluLysAlaGlu 313
RESULT 32
US-09-620-405B-483
; Sequence 483, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 483
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-620-405B-483

Alignment Scores:
Pred. No.:      5,41e-124      Length:      323
Score:          1397.00      Matches:      288
Percent Similarity: 94.50%      Conservative: 4
Best Local Similarity: 93.20%      Mismatches: 13
Query Match:     41.05%      Indels:      5
DB:              4          Gaps:      0

US-09-602-362B-15 (1-2030) x US-09-620-405B-483 (1-323)
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Db      9 GluValSerHisThrHisGluAsnGluAsnTyLeuLeuHisGluAsnCysMetLeuLys 28
QY      1170 AAGGAATTCGCCATGCTAAATCTGAAATAGGCACACTCAAAACACCAATACCAGAAAAG 1229
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Db      29 LysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyGlnGluLys 48
QY      1230 GAAATTAATATCTTTCAGGACATTAAGATTTTAAAGAAAAGAACTGCTGAATTCAGATG 1289
      ::::
Db      49 GluAsnLysTy-PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
QY      1290 ACCCTAAACTGAAGAGGAATCATTAACTAAAGGGCATCTCAATATAGTGGCAGCTT 1349
      ::::
Db      69 ThrLeuLysLeuLysGluSerLeuThrLysA-GAlaSerGlnTySerGlnGlnLeu 68
QY      1350 AAGGTTCTGATAGCTGAGAACCAATGCTCACTTCTTAAATTCAGGAAAAAACAAGACAAA 1409
      ::::
Db      89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY      1410 GAAATCTAGACGCAAAATGGAATCAACACCACTCCTAGACTGGCTTCCTGCTTACAGAC 1469
      ::::
Db      109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128
QY      1470 CATGATCAAAATTCGATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTCAGGAGAT 1529
      ::::
Db      129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY      1530 GCTTGTTCGAAAGAAAATGATGTTGATGTGAGTGTACCGATATATATACAAATGAGGT 1589
      ::::
Db      149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyAsnAsnGluVal 168
QY      1590 GCTCCATCAACACTTTCGAGGCTCAAAAGGAATCCANAAGCCCTAAATAATTAATCTCAA 1649
      ::::
Db      168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188
QY      1650 TTATGAGGAGATGCTCTTAAGAGAAAATACATGTTTCAGGAACATGCACAAAGAGACC 1709
      ::::
Db      188 nTyAlaGlyAspAlaLeuArgGluAsnThrLeuValSer-GluHisAlaGlnArgAspG 208
QY      1710 AACGTGAAACACAGTGTCAAAATGAAGAAGCTGAACACATGTTTCAAAANGAACAGATN 1769
      ::::
Db      208 lnArgGluThrGlnCysGlnMetLysGluAlaGluHisMetTyGlnAsnGluGlnAspA 228
QY      1770 ATGTGAACAAACACACTGANCACAGGAGTCTCTAGATCAGAAATTTATTTCAACTACAAA 1829
      ::::
Db      228 snValAsnLysHisThrGluGlnGlnGluSerLeuAspGlnLysLeuPheGlnLeuGlnS 248
QY      1830 GCAAAAAATATGTGCTTCAACAGCAATTAGTTCATGCACATAANGAAAGCTGCAACAAA 1889
      ::::
Db      248 erLysAsnMetTrpLeuGlnGlnLeuValHisAlaHis-LysLysAlaAspAsnLys 267
QY      1890 AGCAAGATAACAATTGATNTTCATTTCCTGAGAGGAAATGCGN-CATCATCTTCTTAAA 1948
      ::::
Db      268 SerLysIleThrIleAspIleHisPheLeuGluArgLysMetGlnHisLysLeuLys 287
QY      1949 GAGAAAAATCAGGAGATATTTTATTTATACNATAACCATTTAAAAAACCCGTATATTTCAATA 2008
      ::::
Db      288 GluLysAsnGluGluIlePheAsnTyAsnAsnHisLeuLysAsn-ArgIleTyGlnTy 307
QY      2009 TGGAAAAAANAAAAA 2027
      ::::
Db      307 rGluLysGluLysAlaGlu 313

RESULT 33
US-09-604-287A-483
; Sequence 483, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 483
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-604-287A-483

Alignment Scores:
Pred. No.:      5,41e-124      Length:      323
Score:          1397.00      Matches:      288
Percent Similarity: 94.50%      Conservative: 4
Best Local Similarity: 93.20%      Mismatches: 13
Query Match:     41.05%      Indels:      5
DB:              4          Gaps:      0

US-09-602-362B-15 (1-2030) x US-09-604-287A-483 (1-323)
QY      1110 CAGGTTTCTCACACTCATGAAATGAAATTTCTTACATGAAATTCATGTTGAAA 1169
      ::::
Db      9 GluValSerHisThrHisGluAsnGluAsnTyLeuLeuHisGluAsnCysMetLeuLys 28
QY      1170 AAGGAATTCGCCATGCTAAATCTGAAATAGGCACACTGAACCAACCAATACCAGAAAAG 1229
      ::::
Db      29 LysGluLeuAlaMetLeuLysLeuGluLeuAlaThrLeuLysHisGlnTyGlnGluLys 48
QY      1230 GAAATTAATATCTTTCAGGACATTAAGATTTTAAAGAAAAGAACTGCTGAATTCAGATG 1289
      ::::
Db      49 GluAsnLysTy-PheGluAspIleLysIleLeuLysGluLysAsnAlaGluLeuGlnMet 68
QY      1290 ACCCTAAACTGAAGAGGAATCATTAACTAAAGGGCATCTCAATATAGTGGCAGCTT 1349
      ::::
Db      69 ThrLeuLysLeuLysGluSerLeuThrLysA-GAlaSerGlnTySerGlnGlnLeu 68
QY      1350 AAGGTTCTGATAGCTGAGAACCAATGCTCACTTCTTAAATTCAGGAAAAAACAAGACAAA 1409
      ::::
Db      89 LysValLeuIleAlaGluAsnThrMetLeuThrSerLysLeuLysGluLysGlnAspLys 108
QY      1410 GAAATCTAGACGCAAAATGGAATCAACACCACTCCTAGACTGGCTTCCTGCTTACAGAC 1469
      ::::
Db      109 GluIleLeuGluAlaGluIleGluSerHisHisProArgLeuAlaSerAlaValGlnAsp 128
QY      1470 CATGATCAAAATTCGATCAAGAAAAAGTCAAGAACCTGCTTTCCACATTCAGGAGAT 1529
      ::::
Db      129 HisAspGlnIleValThrSerArgLysSerGlnGluProAlaPheHisIleAlaGlyAsp 148
QY      1530 GCTTGTTCGAAAGAAAATGATGTTGATGTGAGTGTACCGATATATATACAAATGAGGT 1589
      ::::
Db      149 AlaCysLeuGlnArgLysMetAsnValAspValSerSerThr-IleTyAsnAsnGluVal 168
QY      1590 GCTCCATCAACACTTTCGAGGCTCAAAAGGAATCCANAAGCCCTAAATAATTAATCTCAA 1649
      ::::
Db      168 IleuHisGlnProLeuSerGluAlaGlnArgLysSerLysSerLeuLysIleAsnLeuAs 188
QY      1650 TTATGAGGAGATGCTCTTAAGAGAAAATACATGTTTCAGGAACATGCACAAAGAGACC 1709
      ::::
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